

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 16, 2004, 05:53:59 ; Search time 3768 Seconds
(without alignment)
10943.977 Million cell updates/sec

Title: US-09-923-236-1

Perfect score: 1008

Sequence: 1 agacagactaaaagccat.....tagataattcagaccatcg 1008

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Genbank1.*
1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_scs.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
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22: em_ov.*
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26: em_ro.*
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28: em_un.*
29: em_vl.*
30: em_hcg_hum.*
31: em_hcg_inv.*
32: em_hcg_other.*
33: em_hcg_mus.*
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35: em_hcg_rtd.*
36: em_hcg_mam.*
37: em_hcg_vrt.*
38: em_sy.*
39: em_hcgo_hum.*
40: em_hcgo_mus.*
41: em_hcgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1008	100.0	1008	6 AR263643	AR263643 Sequence
2	997	98.9	998	6 AX061225	AX061225 Sequence
3	981.6	97.4	1325	6 BD131596	BD131596 Secretory
4	578.4	57.4	96481	9 AC104811	AC104811 Homo sapi
5	575.2	57.1	157836	2 AC060228	AC060228 Homo sapi
6	558	55.4	639	6 BD109282	BD109282 EST and e
7	537.6	53.3	185969	2 AC069037	AC069037 Homo sapi
8	470	46.6	544	6 BD107961	BD107961 EST and e
9	460	45.6	657	6 AR263644	AR263644 Sequence
10	449	44.5	470	6 BD071746	BD071746 Secreted
11	421	41.8	450	6 BD071795	BD071795 Secreted
12	419.4	41.6	185969	2 AC069037	AC069037 Homo sapi
13	339.6	33.7	485	6 BD122986	BD122986 EST and e
14	286.4	28.4	296	6 BD071681	BD071681 Secreted
15	122.6	12.2	259038	2 AC099443	AC099443 Rattus no
16	121.2	12.0	3489	6 AR072952	AR072952 Sequence
17	121.2	12.0	3489	6 AR254713	AR254713 Sequence
18	121.2	12.0	3489	6 AR261360	AR261360 Sequence
19	121.2	12.0	3489	6 AX107938	AX107938 Sequence
20	121.2	12.0	3489	14 KSUS2064	KSUS2064 Kaposi's sa
21	121.2	12.0	32207	6 AR065852	AR065852 Sequence
22	121.2	12.0	32207	6 AR127850	AR127850 Sequence
23	121.2	12.0	32207	6 AR194752	AR194752 Sequence
24	121.2	12.0	137508	14 KSUV5698	KSUV5698 Kaposi's sa
25	117.8	11.7	28559	14 AF148805	AF148805 Kaposi's sa
26	116.6	11.6	1365	10 BC049645	BC049645 Mus muscu
27	115.2	11.4	133661	14 U93872	U93872 Kaposi's sa
28	113.2	11.2	158249	2 AL953878	AL953878 Dantio rer
29	111.4	11.1	293592	2 AC094571	AC094571 Rattus no
30	111	11.0	177100	2 AC112388	AC112388 Rattus no
31	111	11.0	246774	2 AC095078	AC095078 Rattus no
32	110.8	11.0	2931	14 AP192756	AP192756 Kaposi's sa
33	110.6	11.0	5719	10 MNCRTS1	AF051726 Mus muscu
34	110.6	11.0	188880	10 AC092203	AC092203 Mus muscu
35	110.4	11.0	2286	6 AX460942	AX460942 Sequence
36	110.4	11.0	168210	2 AC116700	AC116700 Mus muscu
37	109.6	10.9	224198	2 AC106674	AC106674 Rattus no
38	109.6	10.9	249541	2 AC095672	AC095672 Rattus no
39	109.6	10.9	249774	2 AC126196	AC126196 Rattus no
40	109.4	10.9	272545	2 AC090533	AC090533 Mus muscu
41	109	10.8	182534	10 AC074046	AC074046 Mus muscu
42	108	10.7	186559	10 AL606742	AL606742 Mouse DNA
43	108	10.7	180944	2 AC113108	AC113108 Mus muscu
44	107.8	10.7	178597	10 AL807824	AL807824 Mouse DNA
45	107.8	10.7	238518	2 AC132752	AC132752 Rattus no

ALIGNMENTS

RESULT 1
AR263643
LOCUS AR263643 1008 bp DNA
DEFINITION Sequence 1 from patent US 6331413.
ACCESSION AR263643
VERSION AR263643.1 GI:28075576
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1008)
AUTHORS Adler,D.A. and Sheppard,P.O.
TITLE Secreted salivary Zsig63 Polypeptide
JOURNAL Patent: US 6331413-A 1 18-Dec-2001;
FEATURES Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a


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Db      541 CAGCCACACCTGTAGAGCTGAGCTGCTGCTGAGAGGAGCCCTGTTGAGAGCTGAGCTGCTG 600
Qy      606 CAGAGGACCTGTGTGAGCTGAGCTGCTGCTGAGAGGACCACTGTGTGAGAGCTGAGCTGCTG 665
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Qy      666 CAGAGGACCTGTGTGAGCTGAGCTGCTGCTGAGAGGACCACTGTGTGAGAGCTGAGCTGCTG 725
Db      661 CAGAGGACCTGTGTGAGCTGAGCTGCTGCTGAGAGGACCACTGTGTGAGAGCTGAGCTGCTG 720
Qy      726 CAGCCAGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 785
Db      721 CAGCCAGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Qy      786 GAAATCTCTAGAGAGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 845
Db      781 GAAATCTCTAGAGAGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Qy      846 CTACAAAGCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 905
Db      841 CTACAAAGCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 900
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RESULT 3
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LOCUS      BD131596
DEFINITION      Secretory proteins and polynucleotides encoding the same.
ACCESSION      BD131596
VERSION      BD131596.1 GI:23226541
KEYWORDS      JP 2002503634-A/5.
SOURCE      unidentified
ORGANISM      unidentified
REFERENCE      1 (bases 1 to 1325)
AUTHORS      Jacobs, K., McCoy, J.M., Lavallie, E.R., Racie, L.A., Treac, M.,
      Spaulding, V. and Agostino, M.J.
      Secretory proteins and polynucleotides encoding the same
      Patent: JP 2002503634-A 5 05-FEB-2002;
      GENETICS INSTITUTE INC
TITLE      OS Unidentified
COMMENT      PN JP 2002503634-A/5
      PD 05-FEB-2002
      PF 01-JUL-1998 JP 2000501179
      PR 02-JUL-1997 US 08/887195 27-OCT-1997 US 08/958304 PI
      KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI
      MAURICE TREACY,
      PI VIKKI SPAULDING, MICHAEL J AGOSTINO
      PC C07K14/47, A61K38/00, A61P3/10, A61P7/00, A61P7/02, A61P7/04 PC
      A61P7/06, A61P11/06,
      PC A61P17/02, A61P19/02, A61P19/04, A61P19/10, A61P21/00, A61P21/04,
      PC A61P25/00,
      PC A61P25/14, A61P25/16, A61P25/28, A61P29/00, A61P31/04, A61P31/10,
      PC A61P31/12,
      PC A61P33/00, A61P35/00, A61P35/04, A61P37/04, A61P37/06, A61P37/08,
      PC A61P43/00,
      PC C12N5/10, C12N15/09, C12P21/02, A61K39/395, A61K39/395, A61K37/02,
      PC C12N5/00,
      PC C12N15/00
      CC Strandedness: Double;
      CC Topology: Linear;
      CC Secretory proteins and polynucleotides encoding the same FH
      Key location/Qualifiers
      FT source 1..1325
      FT /organism='Unidentified'.
      FT location/Qualifiers

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Best Local Similarity 99.5%; Pred. No. 3.6e-189;
Matches 995; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
10 AAAAAAGCAGATGATTTCTTTGTTTCTCTTAAAGAAAGAAATATATTTAAAAATAC 69
9 AAAAAAGCAGATGATTTCTTTGTTTCTCTTAAAGAAAGAAATATATTTAAAAATAC 68
70 ATTGCGATTTTCTTAAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 129
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Db 969 TGAATATTAAATTAATTAATGATTAATTAGACCAATGG 1008

RESULT 4	AC104811	AC104811	96481 bp	DNA	linear	PRI 16-APR-2001
LOCUS	AC104811					
DEFINITION	Homo sapiens	BAC clone	Rpl1-653L5	from 4,	complete sequence.	
ACCESSION	AC104811					
VERSION	AC104811.4	GI:19698738				
KEYWORDS	HTG.					
SOURCE	Homo sapiens	(human)				
ORGANISM	Homo sapiens					

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE

Eukaryotic; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 96481)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 96481)
Desai, A., Haakenson, W. and Dignan, G.
The sequence of Homo sapiens BAC clone RP11-653J5
Unpublished (2001)
3 (bases 1 to 96481)
Waterston, R. H.
Direct Submission
Submitted (21-DEC-2001) Genome Sequencing Center, Washington

REFERENCE 4 (bases 1 to 96481)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (14-MAR-2002) Genome Sequencing Center, Washington

REFERENCE 5 (bases 1 to 96481)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-2002) Genome Sequencing Center, Washington

REFERENCE 6 (bases 1 to 96481)
AUTHORS Waterston, R. H.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-2002) Genome Sequencing Center, Washington

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
7 (bases 1 to 96481)	Waterston, R.	Direct Submission	Submitted (16-APR-2002)	Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
			On Mar 24, 2002 this sequence version replaced	ga:19424658.

Center: Washington University Genome Sequencing Center
Genome Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: asplens@wustn.wustl.edu
Summary Statistics
Center project name: H_NH0653L05

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCT-human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P. Y., Zhao, B., Fritgen, E., Tateno, M., Cacanese, J. J. and de Jong, P. J. (1998). An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

PICTOR: PBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-529K3, 2000 bp overlap; the clone sequenced to the right is RP11-719M6, 2000 bp overlap. Actual end of this clone is at base position 35039 of RP11-719M6.

FEATURES

Source

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Matches 624;	Conservative 0;	Mismatches 76;	Indels 0;	Gaps 0;

Qy 199 TGAGATGACAAATGACATGGTACCCACTTCATCCATCTCTGAATATTCCTTATGGCAT 258

Db 60879 TTAGAGATGACAAATGACATGGTACCCACTTCATCCATCTCTGAATATTCCTTATGGCAT 60935

Qy 259 ACGGAATTTACACACTCTCTTTATTTATGGCCAGATGAAATACAGTCCCCAGTTAACCTGG 318

Db	60939	ACGGAATTTTACCACTCTCTCTTTATTATAGCCCAAGTAATACAGTCCCAAGTTACCTCTGG	609988
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Db	60999	GAAATCTTACACTGACAGAGGGTTACCTTGGATCCCTGGATTTCTAATCTTCTGGATT	610588
Qy	379	CCCTTAATGCTATACATCATCGTGGTTTCCCTTAAAGTACTCAAGTTGAATGTTCCCTCT	438
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Qy	439	CCCTCTAAGGGGTTTCCCGTTTGTCCCTCTTCAAGTTTCTTTCAGCAGCTGACAGACC	498
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Qy	499	CGCTGCCCAACCTAATGACAGCTGAGGCTGCTGACGTGACCTCTTACAGCCACACCTGT	558
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Qy	559	AGCAGCTGAGCCTGCTGACAGAGGGCCCTGTGTCAGAGCTGAGCCTGTGACAGAGCACCTGT	618
Db	61239	AGCAGCTGAGCCTGCTGACAGAGGGCCCTGTGTCAGAGCTGAGCCTGTGACAGAGCACCTGT	612988
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Db	61539	ATCTATATCACTTAAATATTTTGAACAGCTTATTTTCAGA	615788

RESULT	5
AC060228	
LOCUS	
DEFINITION	ACO60228 157836 bp DNA linear HTG-08-JAN-2003 Homo sapiens chromosome 4 clone RP11-922D2, WORKING DRAFT SEQUENCE.
ACCSSION	ACO60228
VERSION	ACO60228
KEYWORDS	AC060228..10 GI:20335630
SOURCE	HTG; HTGS PHASEI; HTGS _DRAFT. Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Bakaryofe; Metzger; Chorodeta; Cranata; Vertebrate; Euteleostomi; Mammalia; Euheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 157836) Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen.C., AUTHORS

1 (bases 1 to 157836)

Alzayza, M.; Metazos; Chorodai; Catarrhini; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 157836)

Alzayza, M.; Metazos, C.; Adio-Oduola, B.; Ali-Osman, F.R.; Allen, C.; Alzayza, M.; Alzayza, S.L.; Amaral, H.C.; Aze, J.R.; Ayale, M.; Banks, T.; Banerjee, J.; Benton, J.; Bimsge, K.; Blankenburg, K.; Bonnin, D.; Bouch, J.; Bowles, S.; Brieva, M.; Brown, E.; Brown, M.; Bryant, N.P.; Buhy, C.; Burck, P.; Burdick, C.; Burrell, K.L.; Byrd, N.C.; Carron, T.F.; Carter, M.; Cavazos, S.R.; Chacko, J.; Chavez, D.; Chen, G.; Chen, R.; Chen, Z.; Chowdhry, I.; Christopoulos, C.; Cleveland, C.D.; Cox, C.; Coyle, M.D.; Dathore, S.R.; David, R.; Davila, M.L.; Davis, C.; Davy-Carroll, L.; Dedetich, D.A.; Delavie, K.R.; Delgado, O.; Dunn, A.L.; Ding, Y.; Dinh, H.H.; Douthwaite, K.J.; Draper, H.; Dugan-Rocha, S.; Durbin, K.J.; Earhart, C.; Edgar, D.; Edwards, C.C.; Elhaj, C.; Escoto, M.; Falls, T.; Ferraguto, D.; Flagg, N.; Ford, J.; Foster, P.; Franz, P.; Gabisi, A.; Gao, J.; Garcia, A.; Garner, T.; Garza, N.; Gill, R.; Gorielli, J.H.; Guevara, M.; Gunaratne, P.; Hale, S.; Hamilton, K.; Harris, C.; Harris, K.; Hart, M.; Havlik, P.; Hawes, A.; Hernandez, J.

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 Wu, C., Wu, Y., Wu, Y. P., Zhou, J., Zorilla, S., Nelson, D.,
 Weinstein, G., and Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 157836)
 Worley, K. C.
 Direct Submission
 Submitted (20-APR-2000) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 157836)
 Worley, K. C.
 Direct Submission
 Submitted (08-JAN-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Apr 28, 2002 this sequence version replaced gi:16117945.

 Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

 Project Information
 Center project name: HBBB
 Center clone name: RP11-922D2

 Summary Statistics
 Sequencing vector: M13:
 Chemistry: Dye-terminator Big Dye: 7% of reads
 Chemistry: Dye-terminator Big Dye: 7% of reads
 Assembly program: Phrap; version 0.990139
 Consensus quality: 147257 bases at least Q40
 Consensus quality: 151545 bases at least Q40
 Consensus quality: 153682 bases at least Q20
 Estimated insert size: 166756; sum-of-contigs estimation
 Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

 NOTE: Estimated insert size may differ from sequence length
 (see <http://www.hgsc.bcm.tmc.edu/docs/genbankdraftdata.html>)
 NOTE: This is a 'working draft' sequence. It currently
 consists of 29 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.
 * 1 2348: contig of 2348 bp in length
 * 2349 2448: gap of unknown length
 * 2449 4666: contig of 2218 bp in length
 * 4667 4766: gap of unknown length
 * 4767 6990: contig of 2224 bp in length

[illegible]

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 DB 36031 CCCCTATGAGGGTTTCCGTTGGTTTCCCTTACCTACTCACTGATGATGTTCTTCTCT 36090
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 DB 36091 CCGTGGCCCACTATTTGACAGCTGAGCTGAGCTGACCTCTTACAGCCACACCTGT 36150
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 DB 36211 TGGAGCTGAGCTGCTGACAGGGGCCCCCTGTTGACCTGAGCTGAGCTGAGCCACTGT 36270
 QY 679 TGGAGTGGAGCCAGCTGACAGAGGAACTTACACCACTGAGCTGACAGCCAAAGCTGT 738
 DB 36271 TGGAGTGGAGCCAGCTGACAGAGGAACTTACACCACTGAGCTGACAGCCAAAGCTGT 36330
 QY 739 TGGCCCAAGAACTGACCTCTTCTCTCTCTGTTGAACAGGCA 778
 DB 36331 TGGCCCAAGAACTGACCTCTTCTCTCTCTGTTGAACAGGTA 36370

RESULT 6
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 VERSION BD109282.1
 KEYWORDS JP 2002010789-A/1359.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 639)
 AUTHORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.B.
 TITLE EST and encoded human protein
 JOURNAL Patent: JP 2002010789-A 1359 15-JAN-2002;
 GENSET CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2002010789-A/1359
 PD 15-JAN-2002 JP 20020280989
 PF 07-AUG-2000 JP 20020280989
 PR 05-AUG-1999 US 60/147499
 PI JEAN BAPTISTE DUMAS MIKNE EDWARDS, SEVEILIN JOBERT, JEAN EYE
 GIORDANO
 PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
 C12N1/21,
 PC C12N5/10, C12P21/02, C12P21/08, C12O1/68, C12N15/00, C12N5/00, PC
 C12N15/00
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FEATURES
 source
 BASE COUNT 158 a 164 c 118 g 198 t 1 others

ORIGIN

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 Best Local Similarity 99.3%; Pred. No. 4, 1e-103;
 Matches 580; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

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 QY 61 TAAAAATACATGCTGATTTTCTTAAACAAATTAATTAAGTTAATTTATAGAGTC 120
 DB 118 TAAAAATACATGCTGATTTTCTTAAACAAATTAATTAAGTTAATTTATAGAGTC 177
 QY 121 AATCAAAATGAAGCTTCTCTTGGGCGCTGACATTTGATGTTGCTTTGCAAGAGAG 180
 DB 178 AATCAAAATGAAGCTTCTCTTGGGCGCTGACATTTGATGTTGCTTTGCAAGAGAG 237
 QY 181 ACGTTCCCTTCATTTGAGATGACAAATGAGATGACCACTTCATTCATCTCT 240
 DB 238 ACGTTCCCTTCATTTGAGATGACAAATGAGATGACCACTTCATTCATCTCT 297
 QY 241 GAATATTCCTTATGACATACGAATTTACACCTCTCTTATTTATGCCGAGTAAATAC 300
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 QY 301 AGTCCCAAGTTACCTGGAATATTAACATGACAGAGGTTACCTTGATCCCTGAT 360
 DB 358 AGTCCCAAGTTACCTGGAATATTAACATGACAGAGGTTACCTTGATCCCTGAT 417
 QY 361 TCTAACTTCTCTGATTTCCCTATGTTATGATGATGATGATGATGATGATGATGAT 420
 DB 418 TCTAACTTCTCTGATTTCCCTATGTTATGATGATGATGATGATGATGATGATGAT 477
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 DB 478 GTTGAATGTTCT 537
 QY 481 TTCACAGCTGACAGACCCGCTGACCCCACTTATGACAGCTGACCTGCTGACCTGAC 540
 DB 538 TTCACAGCTGACAGACCCGCTGACCCCACTTATGACAGCTGACCTGCTGACCTGAC 596
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RESULT 7
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 SEQUENCE, 34 unordered pieces.
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 VERSION AC069037.1
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 185969)
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 JOURNAL Unpublished
 TITLE Homo sapiens chromosome 4, clone RP11-653L5
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, P., Boguslavsky, L., Bouhassira, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S., Collimore, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domingo, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Glade, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hages, B., Heford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karas, A.,

TITLE
JOURNAL
COMMENT

Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J.,
Levine, R., Lien, C., Liu, G., Locke, K., MacDonald, P., Margulis, N.,
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O'Neill, D., Ollivar, T.M., Oliver, J., Peterson, K., Pierre, N.,
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Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
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Testaye, S., Theodore, J., Tirrell, A., Travers, M., Triggilio, J.,
Vassiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (17-MAY-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submission@genome.wi.mit.edu

Project Information

Center project name: L7416

Center clone name: 653.L.5

Summary Statistics

Sequencing vector: M13, M77815, 100% of reads

Chemistry: Dye-terminator Big Dye, 100% of reads

Assembly program: Phrap, version 0.960731

Consensus quality: 167163 bases at least Q40

Consensus quality: 175659 bases at least Q30

Consensus quality: 179699 bases at least Q20

Insert size: 18800; agarose-fp

Insert size: 182659; sum-of-coverage

Quality coverage: 3.6 in Q20 bases; sum-of-coverage

Quality coverage: 3.7 in Q20 bases; sum-of-coverage

* NOTE: This is a 'working draft' sequence. It currently
* consists of 34 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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1      1727: contig of 1727 bp in length
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*      6002      6101: gap of 100 bp
*      6102      7881: contig of 1780 bp in length
*      7882      7981: gap of 100 bp
*      7982      10379: contig of 2398 bp in length
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*      10480      13080: contig of 2601 bp in length
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FEATURES

source

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*      98012      103109: contig of 5098 bp in length
*      103110      103209: gap of 100 bp
*      103210      109911: contig of 6702 bp in length
*      109912      110011: gap of 100 bp
*      110012      119453: contig of 9442 bp in length
*      119454      119553: gap of 100 bp
*      119554      126958: contig of 7405 bp in length
*      126959      127058: gap of 100 bp
*      127059      134408: contig of 7350 bp in length
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*      143840      143939: gap of 100 bp
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QY 263 AATTACCACTCTCTTATTAATGCGCCAGTAATACAGTCCCGATTACCTGGGAAT 322
DB 167886 AATTACCACTCTCTTATTAATGCGCCAGTAATACAGTCCCGATTACCTGGGAAT 167827
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DB 167826 ACTTACCTGACACAGGGTACCTTCGTATCCCTGATTTCTTAATCTTCTCTGATTCGCC 167767
QY 383 TATGTCTATCACTCCGTGTTTCCCTTAAGCTACAGTGAATGTTCTCTCTCCCT 442
DB 167766 TATGTCTATCACTCCGTGTTTCCCTTAAGCTACAGTGAATGTTCTCTCTCCCT 167707
QY 443 CCTAGGGGTTTCCGTTTCCCTTCCTCAAGGTTTTTTTACAGCACTGACGACCCGCT 502
DB 167706 CCTA-GGGTTTCCGTTTCCCTTCCTTC-AGGTTTTTTCAGCACTGACGACCCGCT 167649
QY 503 GCCCACTATTGACCTGAGCTGCTGACGCTGACCTCTTACAGCCACACTGTAGCA 562
DB 167648 GCCCACTATTGACCTGAGCTGCTGACGCTGACCTCTTACAGCCACACTGTAGCA 167589
QY 563 GCTGACCTGCTGCAAGGGCCCTGTTGCAAGCTGCTGCTGCAAGGCACTGTTGGA 622
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QY 623 GCTGACCTGCTGCAAGGCACTGTTGCAAGCTGCTGCTGCAAGGCACTGTTGGA 682
DB 167528 GCTGACCTGCTGCAAGGCACTGTTGCAAGCTGCTGCTGCAAGGCACTGTTGGA 167469
QY 683 GTGAGCCAGCTGCAAGAACTTCAACAGCTGACCTGTCAACAGCCAGCTGTGCTC 742
DB 167468 GTGAGCCAGCTGCAAGAACTTCAACAGCTGACCTGTCAACAGCCAGCTGTGCTC 167409
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 VERSION BD107961.1 GI:23202779
 KEYWORDS JP 2002010789-A/38.
 SOURCE
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
 TITLE EST and encoded human protein
 JOURNAL Patent: JP 2002010789-A 38 15-JAN-2002;
 GENSET CORP

COMMENT
 OS Homo sapiens (human)
 PN JP 2002010789-A/38
 PD 15-JAN-2002
 PF 07-AUG-2000 JP 2000280989
 PR 05-AUG-1999 US 60/147499
 PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EYE PI
 GIORANO

PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
 C12N1/21,
 PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
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DB 118 TAAATAATCATTCGTAATTTCTTAAACATTAATTATAGTTTAATATTAGAGGTC 177
QY 121 AATCAAAATGAAGCTTCTCTTGGGCTGCAATCTATAGTTTGTGTTTGAAGAGG 180
DB 178 AATCAAAATGAAGCTTCTCTTGGGCTGCAATCTATAGTTTGTGTTTGAAGAGG 237
QY 181 ACGTTCCCTTCATTGTGAGATGACATGACAGATGTCACCACTTCACTCTCT 240
DB 238 ACGTTCCCTTCATTGTGAGATGACATGACAGATGTCACCACTTCACTCTCT 297
QY 241 GAATATTCCTTAATGACGAAATTTACCACTCTCTTATTTATGCCCAAGTAATAC 300

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Db 298 GAATATTCCTTATGCAATACGGAATTTACCACTCTCTTATTATTCGCCAGTAATAC 357
Qy 301 AGTCCCGATTACCTGGGAATCTTACATGACACAGGGTTACTTGTATCCCTGGAT 360
Db 358 AGTCCCGATTACCTGGGAATCTTACATGACACAGGGTTACTTGTATCCCTGGAT 417
Qy 361 TCTACTCTCTCGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTC 420
Db 418 TCTACTCTCTCGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTC 477
Qy 421 GTTGAATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
Db 478 GTTGAATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 536
Qy 481 TT 482
Db 537 TT 538

RESULT 9
AR263644
LOCUS AR263644 657 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 3 from patent US 6331413.
ACCESSION AR263644
VERSION AR263644.1 GI:28075577
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 657)
TITLE Adler D.A. and Sheppard, P.O.
JOURNAL Secreted salivary ZS1G63 polypeptide
PATENT: US 6331413-A 3 18-DEC-2001;
FEATURES
location/Qualifiers
source
BASE COUNT 72 a 150 c 114 g 65 t 256 others
ORIGIN
Query Match 45.6%; Score 460; DB 6; Length 657;
Best Local Similarity 61.0%; Pred. No. 3,4e-83;
Matches 401; Conservative 103; Mismatches 153; Indels 0; Gaps 0;

Qy 128 ATGAAGCTTCCTCTGCGCGCATGATGATGATGATGATGATGATGATGATGATGATGAT 187
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Qy 188 CCTTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 247
Db 61 CCTTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Qy 248 CCTTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 307
Db 121 CCTTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Qy 308 AGTTCACCTGGGAATCTTACATGACACAGGGTTACTTGTATCCCTGATTCCTGATTC 367
Db 181 AGTTCACCTGGGAATCTTACATGACACAGGGTTACTTGTATCCCTGATTCCTGATTC 240
Qy 368 TCTCTGATTCCTCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTC 427
Db 241 TCTCTGATTCCTCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTC 300
Qy 428 GTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 487
Db 301 GTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
Qy 488 GCTGACAGCACCCTGCGCCACCTATTTGACGCTGACGCTGACGCTGACGCTGACGCTGAC 547
Db 361 GCTGACAGCACCCTGCGCCACCTATTTGACGCTGACGCTGACGCTGACGCTGACGCTGAC 420
Qy 548 GCCACACCTGTAGACAGCTGAGCTGCGAGGGGCCCTGTTGACGCTGAGCTGCTGCA 607
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Db 421 GCNACNCGNNGNCGNACGACGACGACGACGACGACGACGACGACGACGACGAC 480
Qy 608 GAGGACCTGTTGAGAGCTGAGAGCTGCTGACAGAGGACCTGTTGAGAGCTGCTGCA 667
Db 481 GAGGACCTGTTGAGAGCTGAGAGCTGCTGACAGAGGACCTGTTGAGAGCTGCTGCA 540
Qy 668 GAGGACCTGTTGAGAGCTGAGAGCTGAGAGGACCTGACAGGACCTGAGAGCTGCTGCA 727
Db 541 GAGGACCTGTTGAGAGCTGAGAGCTGAGAGGACCTGACAGGACCTGAGAGCTGCTGCA 600
Qy 728 GCCAAGCTGCTGCGCCAGAACCTCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 784
Db 601 GCCAAGCTGCTGCGCCAGAACCTCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 657

RESULT 10
BD071746
LOCUS BD071746 470 bp DNA linear PAT 27-AUG-2002
DEFINITION Secreted expressed sequence tags (ESTs).
ACCESSION BD071746
VERSION BD071746.1 GI:22617349
KEYWORDS JP 2001519667-A/556.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 470)
AUTHORS Jacoby, K., McCoy, J. M., Lavallie, B. R., Racie, L. A., Merberg, D., Treacy, M., Spaulding, V., and Agostino, M. J.
TITLE Secreted expressed sequence tags (ESTs)
JOURNAL Patent: JP 2001519667-A 556 23-OCT-2001;
GENETICS INSTITUTE INC
OS Unidentified
PN JP 2001519667-A/556
PD 23-OCT-2001
PF 10-APR-1998 JP 1998543069
PR 10-APR-1997 US 08/838821
PI KENNETH JACOB, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI DAVID MERBERG,
PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC
C1N15/12, C12N5/10, C07K14/47, C1201/68, A61K38/17 CC Strandedness:
Double;
CC Topology: Linear;
CC Secreted expressed sequence tags (ESTs)
FH Key source location/Qualifiers
FT source 1.470
location/Qualifiers
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location/Qualifiers
1.470
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BASE COUNT 116 a 115 c 83 g 156 t
ORIGIN
Query Match 44.5%; Score 449; DB 6; Length 470;
Best Local Similarity 98.9%; Pred. No. 5,7e-81;
Matches 452; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 11 AAAAAGCAGATATCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 70
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Qy 71 TTGGGATTTTCTTAAACATTAATTAATGATGATTAATTAATTAATTAATTAATTAATG 130
Db 71 TTGGGATTTTCTTAAACATTAATTAATGATGATTAATTAATTAATTAATTAATTAATG 130
Qy 131 AAGCTTCCTCTTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 190
Db 131 AAGCTTCCTCTTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 190
Qy 191 TTCAATGGTGAAGATGACATGACATGATGATGATGATGATGATGATGATGATGATGATGAT 250
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Db      191 TTGATTGGGAGGATGACATGACATGCTGACCCACTTCATCTCTGATATTCCT 250
Qy      251 TATGGCATACGGAATTTACCACTCTCTTATTTATGCGCCAGTAATACAGTCCCACT 310
Db      251 TATGGCATACGGAATTTACCACTCTCTTATTTATGCGCCAGTAATACAGTCCCACT 310
Qy      311 TACCCGGAATTAATCTTACACTGACACAGGGTTACCTTGATCCCTGATTTCTACTTCT 370
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Qy      371 CCGGATTCCTCTATGCTATCATGACATCCGATGTTTCCCTAGCTACTGATTTGAT 430
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Qy      431 CCTCTCTCTCTCTCTAGGGGTTTCCGTTTGTCTCTC 467
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RESULT 11
LOCUS      BD071795          450 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION      Secreted expressed sequence tags (ESTs).
ACCESSION      BD071795
VERSION        BD071795.1 GI:22617398
KEYWORDS       JP 2001519667-A/605.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 450)
AUTHORS        Jacobs,K., McCoy,J.M., Lavallie,E.R., Racie,L.A., Werberg,D.,
               Treacy,M., Spaulding,V. and Agostino,M.J.
               Secreted expressed sequence tags (ESTs)
               Patent: JP 2001519667-A 605 23-OCT-2001;
               GENETICS INSTITUTE INC
COMMENT        OS      unidentified
               PN      JP 2001519667-A/605
               PD      23-OCT-2001
               PF      10-APR-1998 JP 1998543069
               PR      10-APR-1997 US 08/838821
               PI      KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI
               DAVID MERBERG
               PI      MARIE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC
               C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC      Strandedness:
               Double;
               CC      Topology: linear;
               CC      Secreted expressed sequence tags (ESTs)
               FH      key      Location/Qualifiers
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               /db_xref="taxon:32644"

BASE COUNT      112 a      113 c      78 g      147 t

ORIGIN
Query Match      41.8%; Score 421; DB 6; Length 450;
Best Local Similarity 100.0%; Pred No. 2.8e-75;
Matches 421; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      49 AAAAAATATATATATATATATATATATATATATATATATATATATATATATATAT 108
Db      21 AAAAAATATATATATATATATATATATATATATATATATATATATATATATATAT 80
Qy      109 ATTCAATAGGTCATTAATAAGTCTTCTCTTGGGCTGATTTGTTGCTTT 168
Db      81 ATTCAATAGGTCATTAATAAGTCTTCTCTTGGGCTGATTTGTTGCTTT 140
Qy      169 TGCAGAGAGAGAGAGGCTTCCCTTCAATGAGTGAATGACAGAGAGTCAACCAT 228
Db      141 TGCAGAGAGAGAGAGGCTTCCCTTCAATGAGTGAATGACAGAGAGTCAACCAT 200

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Qy      229 TCATCATCTCTGATATATTCCTTATGAGCATACGGAATTTACCACTCTCTTATATG 288
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Qy      289 CCCAGTGAATACAGTCCCCAGTTACCTCGGGAATCTTACACTGACACAGGGTTACTTC 348
Db      261 CCCAGTGAATACAGTCCCCAGTTACCTCGGGAATCTTACACTGACACAGGGTTACTTC 320
Qy      349 GATACCTGATTTCTTAACTTCTCTGATTCCTGATTCCTGATTCATCATCCGATTTTC 408
Db      321 GATACCTGATTTCTTAACTTCTCTGATTCCTGATTCCTGATTCATCATCCGATTTTC 380
Qy      409 CTTACCTACCTGATTTCTTAACTTCTCTGATTCCTGATTCCTGATTTCCGTTTGCCTTC 468
Db      381 CTTACCTACCTGATTTCTTAACTTCTCTGATTCCTGATTCCTGATTTCCGTTTGCCTTC 440
Qy      469 T 469
Db      441 T 441

RESULT 12
LOCUS      AC069037          185969 bp      DNA      linear      HTG 17-MAY-2000
DEFINITION      Homo sapiens chromosome 4 clone RP11-653L5 map 4, WORKING DRAFT
SEQUENCE      34 unordered pieces.
ACCESSION      AC069037
VERSION        AC069037.1 GI:7884885
KEYWORDS       HTG, HTGS_PHASE1, HTGS_DRAFT.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 185969)
AUTHORS        Birren,B., Linton,L., Nusbaum,C. and Lander,E.
               Homo sapiens chromosome 4, clone RP11-653L5
               Unpublished
               2 (bases 1 to 185969)
               Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
               Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
               Boguslavsky,L., Boukhalter,B., Brown,A., Burkett,G.,
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               Dodge,S., Domingo,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
               Galagan,J., Gardyna,S., Glade,S., Goyette,M., Graham,L.,
               Grand-Pierre,N., Grant,G., Hagos,B., Heathford,A., Horton,L.,
               Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kamp,L., Karakas,A.,
               Klein,J., Lacroque,K., Lamazares,R., Landers,T., Lehoczy,J.,
               Levine,R., Liu,C., Liu,G., Locke,K., MacDonald,P., Margolis,N.,
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               Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
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               Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
               Young,G., Zainoun,J., Zimmer,A. and Zody,M.
               Direct Submission
               Submitted (17-MAY-2000) Whitehead Institute/MIT Center for Genome
               Research, 320 Charles Street, Cambridge, MA 02141, USA
               All repeats were identified using RepeatMasker:
               Smit, A.F.A. & Green, P. (1996-1997)
               http://ftp.genome.washington.edu/RM/RepeatMasker.html
               ----- Genome Center
               Center: Whitehead Institute/ MIT Center for Genome Research
               Center code: WIBR
               Web site: http://www-seq.wi.mit.edu
               Contact: sequence_submissions@genome.wi.mit.edu
               ----- Project Information
               Center project name: L7416

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----- Summary Statistics -----
Center clone name: 653 L5
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 167163 bases at least Q40
Consensus quality: 175669 bases at least Q30
Consensus quality: 179699 bases at least Q20
Insert size: 188000; agarose-fp
Insert size: 182669; sum-of-contigs
Quality coverage: 3.6 in Q20 bases; agarose-fp
Quality coverage: 3.7 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 34 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
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1727: contig of 1727 bp in length
1728 1827: gap of 100 bp
1828 3423: contig of 1596 bp in length
3424 3523: gap of 100 bp
3524 6001: contig of 2478 bp in length
6002 6102: gap of 100 bp
6102 7881: contig of 1780 bp in length
7882 7981: gap of 100 bp
7982 10379: contig of 2398 bp in length
10380 10479: gap of 100 bp
10480 13080: contig of 2601 bp in length
13081 13180: gap of 100 bp
13181 15812: contig of 2632 bp in length
15813 15912: gap of 100 bp
15913 18292: contig of 2360 bp in length
18293 18392: gap of 100 bp
18393 20550: contig of 2158 bp in length
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24117 24216: gap of 100 bp
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27084 27183: gap of 100 bp
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68028 68127: gap of 100 bp
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72912 73011: gap of 100 bp
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79147 79246: gap of 100 bp
79247 86421: contig of 7175 bp in length
86422 86521: gap of 100 bp
86522 92006: contig of 5485 bp in length
92007 92106: gap of 100 bp
92107 97911: contig of 5805 bp in length
97912 98011: gap of 100 bp
98012 103109: contig of 5098 bp in length
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FEATURES
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* 119454 119553: gap of 100 bp
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* 126959 127058: gap of 100 bp
* 127059 134408: contig of 7350 bp in length
* 134409 134508: gap of 100 bp
* 134509 143839: contig of 9331 bp in length
* 143840 143939: gap of 100 bp
* 143940 155329: contig of 11390 bp in length
* 155330 155429: gap of 100 bp
* 155430 168024: contig of 12595 bp in length
* 168025 168124: gap of 100 bp
* 168125 185965: contig of 17845 bp in length.
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Matches 420; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 199 TGAGATGAGAAAGACATGTCACCCACTTCATTCCTGTAATTCCTATGACAT 258
DB 67607 TTAGAGAGACAAAGACATGTCACCCACTTCATTCCTGTAATTCCTATGACAT 67666
QY 259 ACCGAATTTACCACTCTCTTTATTCAGCCAGTAATACAGTCCCGAGTACCCTGG 318
DB 67667 ACCGAATTTACCACTCTCTTTATTCAGCCAGTAATACAGTCCCGAGTACCCTGG 67726
QY 319 GAATACTTACATGACACAGGGTTTACCTTCGTATCCCTGATTCCTTCTGAGATT 378
DB 67727 GAATACTTACATGACACAGGGTTTACCTTCGTATCCCTGATTCCTTCTGAGATT 67786
QY 379 CCCCTATGCTATCAATCCGAGTTTTCCTTAGCTACTGATGAATGTCCTCTCT 438
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QY 439 CCTCTAGAGGGTTTCCCGTTTCCCTCAAGTTTTCAGAGCTGACAGACC 498
DB 67847 CCTCTAGAGGGTTTCCCGTTTCCCTCAAGTTTTCAGAGCTGACAGACC 67906
QY 499 CGCTGCCACCTATTCAGCTGAGCTGCTGACAGCTCTTACAGCCACACTGT 558
DB 67907 CGCTGCCACCTATTCAGCTGAGCTGCTGACAGCTCTTACAGCCACACTGT 67966
QY 559 AGAGCTGAGCCCTGTCAGAGGGCCCTGTTGACAGCTGAGCCGTCAGAGCACTGT 618
DB 67967 AGAGCTGAGCCCTGTCAGAGGGCCCTGTTGACAGCTGAGCCGTCAGAGCACTGT 68026
QY 619 T 619
DB 68027 T 68027

RESULT 13
LOCUS BD122986 485 bp DNA linear PAT 18-SEP-2002
DEFINITION EST and encoded human protein.
ACCESSION BD122986
VERSION BD122986.1 GI:23217931
KEYWORDS JP 2002010789-A/15063.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukayocsa, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 485)
AUTHORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.B.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 15063 15-JAN-2002;
GENSET CORP
COMMENT OS Homo sapiens (human)
PN JP 2002010789-A/15063
PD 15-JAN-2002
PR 07-AUG-2000 JP 2002080989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EYE PI
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00
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FH Key Location/Qualifiers
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Best Local Similarity 96.4%; Pred. No. 9.7e-59;
Matches 345; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

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QY 230 CATTCATCTCTGAAATTCCTTATGACATAGGAAATTAACACCTCTCTTATTAATGC 289
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QY 410 TTAGCTACTGATTAATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 469
DB 368 TTAGCTACTGATTAATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 427
QY 470 TCAAGGTTTTTTCAGACAGCTGACAGACCCGCTGCCCACTATTCAGCTGAGCTG 527
DB 428 TCAAGGTTTTTTCAGACAGCTGACAGACCCGCTGCTGCTCTCTCTCTCTCTCTCTCT 485

RESULT 14
LOCUS BD071681 296 bp DNA linear PAT 27-AUG-2002
DEFINITION Secreted expressed sequence tags (sests).
ACCESSION BD071681
VERSION BD071681.1 GI:22617284
KEYWORDS JP 2001519667-A/491.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 296)
AUTHORS Jacobs, K., McCoy, J.M., Lavallie, E.R., Racie, L.A., Merberg, D.,
Trecay, M., Spaulding, V. and Agostino, M.J.
TITLE Secreted expressed sequence tags (sests)
JOURNAL Patent: JP 2001519667-A 491 23-OCT-2001;
GENETICS INSTITUTE INC
COMMENT OS Unidentified
PN JP 2001519667-A/491
PD 23-OCT-2001
PR 10-APR-1998 JP 1998543069
PR 10-APR-1997 US 08/838821
PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI
DAVID MERBERG,
PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC
C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness:
Double;
CC Topology: linear;
CC Secreted expressed sequence tags (sests)
FH Key Location/Qualifiers
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BASE COUNT      50 a 99 c 82 g 65 t
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Best Local Similarity 99.7% Prid. No. 6e-48;
Matches 287; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 449 GGTTCCTCCGTTTCCTCCCTTCAGAGTTTTCAGAGCTGACAGACCCCGTGCCTCA 508
DB 1 GGTTCCTCCGTTTCCTCCCTTCAGAGTTTTCAGAGCTGACAGACCCCGTGCCTCA 60
QY 509 CCTATTGACAGTACGCTGCTGACGCTGACCTCTTACAGCCACACCTGTAGACGCTGAG 568
DB 61 CCTATTGACAGTACGCTGCTGACGCTGACCTCTTACAGCCACACCTGTAGACGCTGAG 120
QY 569 CCGTCGTGACAGGAGGCGGCTGTTGACAGCTGACCTGCTGACAGGACACCTGTTGAGCTGAG 628
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QY 629 CCGTCGTGACAGGACACCTGTTGACAGCTGACGCTGCTGACAGGACACCTGTTGAGCTGAG 688
DB 181 CCGTCGTGACAGGACACCTGTTGACAGCTGACGCTGCTGACAGGACACCTGTTGAGCTGAG 240
QY 689 CCAAGCTGACAGAGACCTTACACAGCTGACGCTGCTACAGCCAGGCT 736
DB 241 CCAAGCTGACAGAGACCTTACACAGCTGACGCTGCTACAGCCAGGCT 288

RESULT 15
AC099443/c 259038 bp DNA linear HTG 10-MAY-2003
LOCUS Rattus norvegicus clone CH230-19701, *** SEQUENCING IN PROGRESS
DEFINITION
AC099443
AC099443.5 GI:30521301
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 259038)
Muzny,D.,Marie, W.,Metzker, W.,Lee, A.,Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Albrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Ayagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenship, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Butrell, K., Calderon, B.,
Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
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Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guayra, W.,
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Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolyvet, A.,
Karachay, S., Kelly, S., Kelly, S., Khan, Z., King, J., Kovar, C.,
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Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
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Mawlin, S., McLeod, M. P., McNeill, T. Z., Meenen, B.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L.,

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL
TITLE
JOURNAL
COMMENT
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Pascariu, O., Okunou, G., Olariu, A., Pal, S., Parks, K.,
Pasernak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
Plopper, F., Poldinger, A., Popovic, D., Prims, E., Fu, L.,
Puzo, M., Qutro, J., Rachin, E., Reeves, K., Regier, M. A., Reigh, R.,
Rell, B., Rell, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ritz, S. J.,
Sanders, M., Savary, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C. D., Smaj, D.,
Sneed, A., Sodergren, B., Song, X., Z., Sorelle, R., Soza, J.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usman, K.,
Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J.,
Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wiczyk, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
Weinstock, G. and Gibbs, R. A.
Direct Submission
2 (bases 1 to 259038)
Morley, K. C.
Direct Submission
Submitted (15-NOV-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 259038)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:2364454.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: CH230-19701
Center clone name: Summary Statistics
Assembly program: Atlas 3.0
Consensus quality: 237512 bases at least Q40
Consensus quality: 237879 bases at least Q30
Consensus quality: 240733 bases at least Q20
Estimated insert size: 249015; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 244738: contig of 244738 bp in length

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: January 16, 2004, 05:51:13 : Search time 336 seconds
(without alignments)
8098.314 Million cell updates/sec

Title: US-09-923-236-1

Perfect score: 1008
Sequence: 1 agacagacacaaaagcatc.....tagataatttagacacatg 1008

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 25527561 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1008	100.0	1008	24	AAD45050 Human zslg63 DNA.
2	1008	100.0	1008	24	ABBS2633 DNA encoding human
3	1008	100.0	1008	24	AA820591 Human zslg63 CDNA.
4	1008	100.0	1008	25	ABX93594 Human CDNA encodin
5	997	98.9	998	22	AA272729 Human transport pr
6	981.6	97.4	1325	20	AAV80740 Human secreted pro
7	896.4	88.9	959	20	AAK61352 DNA encoding a hum
8	460	45.6	657	24	AAD45051 Human zslg63 degen

9	460	45.6	657	24	ABBS2634
10	460	45.6	657	24	AA820592
11	460	45.6	657	25	ABX93595
12	449	44.5	470	20	AAV89597
13	421	41.8	450	20	AAV89646
14	286.4	28.4	296	20	AAV89532
15	121.2	12.0	3489	22	AAK30290
16	121.2	12.0	3489	22	AAK82901
17	121.2	12.0	3489	24	ABX93487
18	121.2	12.0	32207	20	AAV73805
19	121.2	12.0	137507	19	AAV19941
20	106	10.5	5120	22	AAK84677
21	100	9.9	1037	21	AAAS9242
22	100	9.9	1472	21	AAAS9241
23	99.2	9.8	1159	24	AAAS9240
24	98.2	9.7	2108	24	ABL67774
25	93.6	9.3	397	20	AAK89891
26	92.8	9.2	5120	22	AAK84677
27	92.4	9.2	1101	22	AAK06303
28	92	9.1	543	13	AAQ23092
29	89.8	8.9	877	24	AB21932
30	89.8	8.9	3042	23	ABL28445
31	89.8	8.9	5215	23	ABL28444
32	88.4	8.8	403	21	ABK10240
33	88.2	8.8	627	23	AA93555
34	87.6	8.7	234	16	AAQ84832
35	87.6	8.7	1101	22	AAK06303
36	86.6	8.6	786	17	AAK46148
37	86.6	8.6	786	20	AAK10978
38	86.4	8.6	486	22	AAK75507
39	85.2	8.5	799	21	AAV55831
40	85.2	8.5	1926	21	AAAS0254
41	85.2	8.5	1926	22	AAK82902
42	85.2	8.5	2580	21	AAK75454
43	85.2	8.5	2580	24	AAK64275
44	85.2	8.5	5452	20	AAK90923
45	85.2	8.5	8705	20	AAK233778

ALIGNMENTS

RESULT 1	
ID	AAD45050
	AAD45050 standard; DNA; 1008 BP.
XX	
AC	AAD45050;
XX	
DT	27-DEC-2002 (first entry)
XX	
DE	Human zslg63 DNA.
XX	
KW	Human; secreted salivary protein; zslg63 protein; host defense protein;
KW	immune modulating factor; antipathogenic; cell-cell signalling molecule;
KW	growth factor; cytokine; growth factor hormone activity; dental carrier;
KW	infection; tooth decay; periodontal disease; gastrointestinal disease;
KW	churn; urinary tract infection; vaginal infection; diabetes; obesity;
KW	anti-inflammatory; chronic tissue damage; lung dysfunction; restenosis;
KW	gene therapy; salivary gland dysfunction; prostate gland dysfunction;
KW	forensic DNA profiling; chondrosarcoma; atherosclerosis; chromosome 4;
OS	gene; de.
XX	
OS	Homo sapiens.
XX	
PH	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	/*tag= a
FT	/product= "Human zslg63 protein"
FT	sig_peptide
FT	128..172
FT	/*tag= b
FT	mat_peptide
FT	173..784
FT	/*tag= c
FT	/product= "Mature human zslg63 protein"

Human secreted sal
Human zslg63 degen
Human zslg63 degen
EST clone CP251.
EST clone CP116.
Kaposi's sarcoma-a
Nucleotide sequenc
Kaposi's sarcoma-a
KSHV LTR DNA (nucl
KSHV long unique c
DNA sequence of hu
Exons B, C and A o
An EcoRI fragment
Oesophagus cancer
Spinocherebellar at
DNA sequence of hu
Human CDNA clone H
Antigen tc-7a gene
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Drosophila melanog
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Trinucleotide repe
DNA encoding novel
Spinocherebellar at
Human CDNA clone H
T. cruzi L19E homo
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Polyglutamine trac
Nucleotide sequenc
Epstein Barr virus
EBV tethering prot
Nucleotide sequenc
Epstein-Barr virus
Anti-sense strand
Vector pShuttle DN

XX US2002090677-A1.
 XX 11-JUL-2002.
 XX 03-AUG-2001; 2001US-0923236.
 XX 17-MAR-1999; 99US-124820P.
 XX 17-MAR-2000; 2000US-0527345.
 XX
 XX (ADLER) ADLER D A.
 XX (SHEP) SHEPPARD P O.
 XX
 XX Adler DA, Sheppard PO;
 XX
 XX MPI: 2002-642378/69.
 XX P-PsDB; AAE27862.
 XX
 XX Novel secreted salivary polypeptide, zslg63, useful as antimicrobial
 XX agent for treating microbial infection, dental caries, periodontal
 XX disease, thrush gastrointestinal disease, and for aiding digestion -
 XX
 XX Claim 3, Page 27-28; 33pp; English.

CC The invention relates to human secreted salivary polypeptide designated
 CC as zslg63 and nucleic acid molecules encoding such polypeptides. zslg63
 CC can be used in detecting agonists and antagonists of its activity, and
 CC is also useful as a host defense polypeptide, immune modulating factor,
 CC antipathogenic polypeptide, cell-cell signalling molecule, growth factor,
 CC cytokine, or as secreted extracellular matrix associated proteins with
 CC growth factor hormone activity. It is useful for treating conditions
 CC associated with pathological microbes, including bacterial, fungal and
 CC viral infections, for treating dental caries (tooth decay), periodontal
 CC disease, thrush and gastrointestinal disease, for treating urinary tract
 CC infection, vaginal infection and for preventing infection in skin and
 CC other epithelial wounds. zslg63 is useful for establishing normal
 CC microflora and protect against pathogenic colonisation and invasion, for
 CC treating chronic tissue damage e.g. damage in extremities associated
 CC with diabetes and useful as anti-inflammatory agents. It is useful as a
 CC marker of lung dysfunction, salivary gland dysfunction, or dysfunction of
 CC prostate gland. It is also therapeutically useful for aiding digestion.
 CC Polynucleotides of the invention are used in gene therapy for increasing
 CC or inhibiting zslg63 activity, for detecting abnormalities on human
 CC chromosome 4 associated with disease or other human traits and as
 CC diagnostic in forensic DNA profiling. Sequences of the invention are
 CC useful for stimulating proliferation or differentiation of cardiac
 CC myocytes, for proliferation or differentiation of adipocytes and for
 CC inhibiting chondrosarcomas, atherosclerosis, restenosis and obesity.
 CC The present sequence is human zslg63 DNA. zslg63 gene is located on
 CC chromosome 4.
 CC
 CC Sequence 1008 BP; 257 A; 251 C; 193 G; 307 T; 0 other;

Query Match 100.0%; Score 1008; DB 24; Length 1008;
 Best Local Similarity 100.0%; Pred. No. 3.5e-207;
 Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGACGACCTAAAGGACGATGATCTTCTGTTCTCTAAAGAGAAATATATTT 60
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 QY 181 ACGGTTCCCTTCATTTGATGAGATGACATGATGATGATGATGATGATGATGAT 240
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 QY 421 GTTGAATGTTCT 480
 DB 421 GTTGAATGTTCT 480
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 DB 481 TTCAAGACCTGACAGACCTGACAGCTGACAGCTGACAGCTGACAGCTGACAGCT 540
 QY 541 TCTTACAGCCACACCTGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 600
 DB 541 TCTTACAGCCACACCTGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 600
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 DB 841 GAATCTTCAAAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
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 QY 961 AAAAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1008
 DB 961 AAAAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1008

RESULT 2
 ABS52633
 ID ABS52633 standard; DNA; 1008 BP.

XX ABS52633;
 XX 15-NOV-2002 (first entry)
 XX
 XX DNA encoding human secreted salivary protein zslg63.
 XX Human; secreted salivary protein; zslg63; immunogen; zslg63-cytokine;
 XX antibody-cytokine; in vivo killing; pathological microbe; bacteria;
 XX fungal; viral; infection; salivary gland; anti-microbial; dental caries;
 XX tooth decay; periodontal disease; thrush; gastrointestinal disease;
 XX urinary tract infection; vaginal infection; skin infection; microflora;
 XX epithelial wound; pathogenic colonisation; invasion; pro-inflammatory;
 XX chronic tissue damage; vascular system; diabetes; anti-inflammatory;
 XX incompetent immune system; AIDS; acquired immunodeficiency syndrome;
 XX chemotherapy; radiation treatment; lung infection; cystic fibrosis;
 XX digestion; chromosome 4; gene; db.

XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 128..787
 FT /tag= a
 FT /product= "Human secreted salivary protein zsig63"
 FT misc_feature 128..784
 FT /tag= b
 FT /note= "Specifically claimed in claim 3"
 FT misc_feature 173..784
 FT /tag= c
 FT /note= "Specifically claimed in claim 3"
 FT US2002081701-A1.
 XX
 XX 27-JUN-2002.
 XX
 XX 03-AUG-2001; 2001US-0922480.
 XX
 XX 17-MAR-1999; 99US-124820P.
 XX 17-MAR-2000; 2000US-0527345.
 XX
 XX (ADLER/) ADLER D A.
 XX (SHEP/) SHEPPARD P O.
 XX Adler DA, Sheppard PO;
 XX WPI; 2002-635468/68.
 XX P-PSDB; ABG31608.
 XX
 PT Novel secreted salivary protein, zsig63 and polynucleotide encoding it
 PT useful for treating microbial infections, inflammatory conditions,
 PT dental caries and lung infections associated with cystic fibrosis
 XX
 XX Claim 3; Page 27-28; 33pp; English.
 XX
 XX The present invention relates to a new secreted salivary protein, zsig63.
 XX The invention is useful for detecting in a test sample, the presence of
 XX an antagonist or agonist of zsig63 protein activity. The invention is
 XX also useful as an immunogen for producing an antibody to zsig63
 XX polypeptide. zsig63-cytokine fusion proteins or antibody-cytokine fusion
 XX protein are useful for enhancing in vivo killing of target tissues.
 XX Pharmaceutical composition comprising purified zsig63 polypeptide are
 XX useful in the treatment of conditions associated with pathological
 XX microbes, including bacterial, fungal and viral infections. High
 XX expression of zsig63 in salivary gland suggests that anti-microbial
 XX polypeptides are useful for treatment of dental caries (tooth decay),
 XX periodontal disease, thrush and gastrointestinal disease. Other
 XX applications can be used in urinary tract infections, vaginal infections,
 XX prevention of infection in skin and other epithelial wounds. The
 XX polypeptide can be used to establish normal microflora and protect
 XX against pathogenic colonization and invasion. The invention is useful
 XX when pro-inflammatory activity is desired. Applications for
 XX such pro-inflammatory activity include the treatment of chronic tissue
 XX damage, particularly in areas having a limited or damaged vascular system
 XX e.g., damage in extremities associated with diabetes. Antagonists to
 XX zsig63 polypeptides may be useful as anti-inflammatory agents. The
 XX invention is useful for the treatment of patients having incompetent
 XX immune system, such as AIDS (acquired immunodeficiency syndrome) patients
 XX or individuals that have undergone chemotherapy, radiation treatment. The
 XX invention is also useful for the treatment of lung infections associated
 XX with cystic fibrosis and its agonists or antagonists are useful for
 XX aiding digestion. The present nucleic acid sequence represents the human
 XX zsig63 gene located on chromosome 4. This sequence encodes the human
 XX secreted salivary protein zsig63 of the invention.
 XX
 XX Sequence 1008 BP; 257 A; 251 C; 193 G; 307 T; 0 other;

Query Match 100.0%; Score 1008; DB 24; Length 1008;
 Best Local Similarity 100.0%; Pred. No. 3.5e-207;
 Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGACAGACTTAAAAAGCCATGATTCCTTCGTTCTCTCTAAAGAGAAAAATTAATT 60
 DB 1 AGACAGACTTAAAAAGCCATGATTCCTTCGTTCTCTCTAAAGAGAAAAATTAATT 60
 QY 61 TAAAAATACATGCGTATTTTCTAAAAACAATAATTATAGTTTAATTGCTAGGGTC 120
 DB 61 TAAAAATACATGCGTATTTTCTAAAAACAATAATTATAGTTTAATTGCTAGGGTC 120
 QY 121 AATCAAAATGAAGCTTCCTTCGTTGGCCGTCATTTGATGTGCTTTTGCAGAGAGAG 180
 DB 121 AATCAAAATGAAGCTTCCTTCGTTGGCCGTCATTTGATGTGCTTTTGCAGAGAGAG 180
 QY 181 ACGGTTCCCTTCATTTGGTGAAGATGACATGACATGCGGTTTCCCTTACCTCACTCT 240
 DB 181 ACGGTTCCCTTCATTTGGTGAAGATGACATGACATGCGGTTTCCCTTACCTCACTCT 240
 QY 241 GAATATTCCTTATGCGATACGGAATTTACACCTCTCTTATATAGCCGATGAAATC 300
 DB 241 GAATATTCCTTATGCGATACGGAATTTACACCTCTCTTATATAGCCGATGAAATC 300
 QY 301 AGTCCCACTTACCTCGGATATCTTACATGACACAGGGTTACCTTCGATCCCGAT 360
 DB 301 AGTCCCACTTACCTCGGATATCTTACATGACACAGGGTTACCTTCGATCCCGAT 360
 QY 361 TCTAATCTCTCGATTCCTCGATATGCTATGACATCGGTTTCCCTTACCTCACTCA 420
 DB 361 TCTAATCTCTCGATTCCTCGATATGCTATGACATCGGTTTCCCTTACCTCACTCA 420
 QY 421 GTTGAATGTTCT 480
 DB 421 GTTGAATGTTCT 480
 QY 481 TTCAGAGCTGAGACACCGCTGCCCCCACTTATGAGCTGAGCTGAGCTGACACC 540
 DB 481 TTCAGAGCTGAGACACCGCTGCCCCCACTTATGAGCTGAGCTGAGCTGACACC 540
 QY 541 TCTTACAGCCACCTGTAGACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 600
 DB 541 TCTTACAGCCACCTGTAGACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 600
 QY 601 TGTGTAGAGGACCTCTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 660
 DB 601 TGTGTAGAGGACCTCTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 660
 QY 661 TGTGTAGAGGACCTCTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 720
 DB 661 TGTGTAGAGGACCTCTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 720
 QY 721 TGTGTAGAGGACCTCTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 780
 DB 721 TGTGTAGAGGACCTCTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 780
 QY 781 TCAATGAATTCCTTGAAGAGATGAGTGAAGTCAATTCCTTGAAGAGATGAGTGAAG 840
 DB 781 TCAATGAATTCCTTGAAGAGATGAGTGAAGTCAATTCCTTGAAGAGATGAGTGAAG 840
 QY 841 GAAATCAAAAGTTTCTTTCTTTTCCAAAGACTTATTCATTCCTGTGTATTCAGAGT 900
 DB 841 GAAATCAAAAGTTTCTTTCTTTTCCAAAGACTTATTCATTCCTGTGTATTCAGAGT 900
 QY 901 ATTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 960
 DB 901 ATTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 960
 QY 961 AAAAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1008
 DB 961 AAAAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1008

RESULT 3
 AAS20591
 ID AAS20591 standard; cDNA; 1008 BP.
 XX

AC	AAS20591;
XX	
DT	23-APR-2002 (first entry)
XX	
DE	Human zsi163 cDNA.
XX	
KW	Human; zsi163; chromosome 4q12-q413; salivary protein; antimicrobial; ss;
KM	microbial infection; tooth decay; periodontal disease; thrush; emphysema;
KW	gastrointestinal disease; urinary tract infection; vaginal infection;
KM	skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;
KM	chronic immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;
XX	acquired bronchitis; gene therapy; protein therapy; gene.
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	128..787
FT	/tag= a
FT	/product= "Human zsi163"
XX	
PN	US6331413-B1.
XX	
PD	18-DEC-2001.
XX	
PF	17-MAR-2000; 2000US-0527345.
XX	
PR	17-MAR-1999; 99US-124820P.
XX	
PA	(ZYMO) ZYMOGENETICS INC.
XX	
PI	Adler DA, Sheppard FO;
XX	
DR	WP1; 2002-096707/13.
DR	P-PSDB; AAU74536.
XX	
PT	Polynucleotides encoding salivary proteins useful as anti-microbial
PT	agents -
XX	
XX	Claim 2; Column 47-50; 29pp; English.
XX	
CC	The invention relates to a polynucleotide derived from the 4q12-q413
CC	region of human chromosome 4 and encoding a zsi163 polypeptide, a
CC	secreted salivary protein with anti-microbial activity, due to their
CC	microbial activity, the sequences can be used in the study of microbial
CC	infections, e.g. For recombinant production of anti-microbial proteins.
CC	The sequences can be used in the treatment of tooth decay, periodontal
CC	disease, thrush, gastrointestinal disease, urinary tract infections,
CC	vaginal infections, skin infections, epithelial wounds, chronic tissue
CC	damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung
CC	infections, sarcoidosis, emphysema and chronic bronchitis. This sequence
CC	represents cDNA encoding human zsi163.
SQ	
	Sequence 1008 BP; 257 A; 251 C; 193 G; 307 T; 0 other;
	Query Match 100.0%; Score 1008; DB 24; Length 1008;
	Best Local Similarity 100.0%; Pred. No. 3.5e-207;
	Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 AGACAGACTTAAAAAAAGCATTATTCCTTGTTCTCTTAAGAAGAAAATAATTT 60
Db	1 AGACAGACTTAAAAAAAGCATTATTCCTTGTTCTCTTAAGAAGAAAATAATTT 60
OY	TAAAAATCATGCGGTATTTTTCTTAAACAATTAATTATAGGTAAATTCATAGGGCT 120
Db	61 TAAAAATCATGCGGTATTTTTCTTAAACAATTAATTATAGGTAAATTCATAGGGCT 120
OY	121 AATCAAAATGAAGCTTCTTCCTTTGGGCCCTGCATTGTATGTGTGCTTTTGAAGAAGAG 180
Db	121 AATCAAAATGAAGCTTCTTCCTTTGGGCCCTGCATTGTATGTGTGCTTTTGAAGAAGAG 180
OY	181 ACGGTTCCTTCATTGTGAGAGATGACAAATGACATGTCACCACTTCAATCCATCTCT 240
Db	181 ACGGTTCCTTCATTGTGAGAGATGACAAATGACATGTCACCACTTCAATCCATCTCT 240

OY	241	GAATATTCCTTATGGCAACGAAATTACACCTCCTCTTTATTTATCGCCAGTGAATAC	300		
OY	241	GAATATTCCTTATGGCAACGAAATTACACCTCCTCTTTATTTATCGCCAGTGAATAC	300		
Db	241	GAATATTCCTTATGGCAACGAAATTACACCTCCTCTTTATTTATCGCCAGTGAATAC	300		
OY	301	AGTCCCAAGTTACCTCGGAAATTAATTACACTGACACAGGGTTACTTGGTATCCCTGGAT	360		
Db	301	AGTCCCAAGTTACCTCGGAAATTAATTACACTGACACAGGGTTACTTGGTATCCCTGGAT	360		
OY	361	TCTAATCTCTCTGGAATTCCTCATAGTCATACATCCGCGGTTTCCCTTAGCTACTCA	420		
OY	421	GTTGAAATTTCTCTCTCTCCCTCCTAGGGGTTTCCCGTTGTCCCTCTTCAAGGTTTTT	480		
Db	421	GTTGAAATTTCTCTCTCTCCCTCCTAGGGGTTTCCCGTTGTCCCTCTTCAAGGTTTTT	480		
OY	481	TTTCAGACCTGACAGACCCCGCTGCCACCTAATTGACGTAGAGCTGTCAGCTGACCC	540		
Db	481	TTTCAGACCTGACAGACCCCGCTGCCACCTAATTGACGTAGAGCTGTCAGCTGACCC	540		
OY	541	TCTTACAGCCACACCTGTAGACGTGAGCCGTGACAGGGGCCCCGTGTGACGTAGCC	600		
Db	541	TCTTACAGCCACACCTGTAGACGTGAGCCGTGACAGGGGCCCCGTGTGACGTAGCC	600		
OY	601	TGCTGACAGGACACCTGTTTGGAGCTGACCTGCTCAGAGGACCTGTTCAGCTAGCC	660		
Db	601	TGCTGACAGGACACCTGTTTGGAGCTGACCTGCTCAGAGGACACCTGTTCAGCTAGCC	660		
OY	661	TGCTGACAGGACACCTGTTTGGAGCTGAGCCAGCTGACAGAACTTCAACAGCTAGCC	720		
Db	661	TGCTGACAGGACACCTGTTTGGAGCTGAGCCAGCTGACAGAACTTCAACAGCTAGCC	720		
OY	721	TGCTACAGCCCAAGCCTGTGCCCCAGAACCTCAACCCCTCTCCCTCTTGAACAGGCAAA	780		
Db	721	TGCTACAGCCCAAGCCTGTGCCCCAGAACCTCAACCCCTCTCTTGAACAGGCAAA	780		
OY	781	TCAGTGAATTCCTCAGAAAGATACATAGGTTTCATTTCTATACGATGACAGAAATTAAGT	840		
Db	781	TCAGTGAATTCCTCAGAAAGATACATAGGTTTCATTTCTATACGATGACAGAAATTAAGT	840		
OY	841	GAAATCTACAAAAGTTTCTTTCTTTCCAAAGACATATTCATTCGTGTGATTCAGAGT	900		
Db	841	GAAATCTACAAAAGTTTCTTTCTTTCCAAAGACATATTCATTCGTGTGATTCAGAGT	900		
OY	901	ATTGATCTCATACTATGATTTGTTTGTGATGTTTTCCTGGAAGTTAATTATTTAGA	960		
Db	901	ATTGATCTCATACTATGATTTGTTTGTGATGTTTTCCTGGAAGTTAATTATTTAGA	960		
OY	961	AAAAACATTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1008		
Db	961	AAAAACATTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1008		
RESULT 4					
ABX93594 standard, cDNA, 1008 BP.					
AC	ABX93594;				
XX	28-MAY-2003	(first entry)			
XX	Human cDNA encoding zslg63.				
DE					
XX	Human, ss; gene, zslg63; adhesin; salivary gland; dental carries; periodontal disease; thrush; gastrointestinal disease; epithelial wound; urinary tract infection; vaginal infection; skin infection; pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS; lung infection; cystic fibrosis; lung dysfunction; digestive; salivary gland carcinoma; Pneumocystis carinii infection; emphysema; chronic bronchitis; prostate dysfunction; prostate adenocarcinoma; cell culture media; gene therapy; human chromosome 4q12-q13; dentinogenesis imperfecta; dentin dysplasia type II.				

XX Homo sapiens.
 OS Location/Qualifiers
 XX Key 128..787
 FT /tag= a
 FT /product= "zsig63"
 FT /note= "this CDS (minus the stop codon) is claimed in
 claim 3"
 FT sig_peptide 128..172
 FT /tag= b
 FT mat_peptide 173..784
 FT /tag= c
 FT /label= Mature zsig63
 FT /note= "this region is claimed in claim 3"
 XX US2002173027-A1.
 XX 21-NOV-2002.
 XX 03-AUG-2001; 2001US-0922469.
 XX 17-MAR-1999; 99US-124820P.
 XX 17-MAR-2000; 2000US-0527345.
 XX (ADLER/) ADLER D A.
 XX (SHEP/) SHEPPARD P O.
 XX Adler DA, Sheppard PO,
 PI MPI; 2003-328428/31.
 XX P-PsDB; AB008515.
 XX Novel isolated zsig63 polypeptide, member of the adhesin family, useful
 PT for treating dental caries, periodontal disease, thrush,
 PT gastrointestinal disease, urinary tract infections, vaginal infections,
 PT skin infections -
 XX Claim 3; Page 26-27; 32pp; English.
 XX The invention relates to an isolated zsig63 polypeptide comprising at
 CC least 90% identity to an amino acid sequence which comprises domain 1 of
 CC zsig63, domain 2, domain 3, mature zsig63 and full length zsig63. Also
 CC included are the polynucleotide encoding zsig63, a zsig63 expression
 CC vector, a cultured cell comprising the vector and expressing the protein,
 CC a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37,
 CC 38-126, 127-219 or 16-219 of zsig63 and an additional protein), using a
 CC zsig63 reporter gene construct to identify zsig63 agonists, and
 CC producing an anti-zsig63 antibody using zsig63 immunogenic peptides,
 CC zsig63 is useful for detecting in a test sample, the presence of
 CC antagonist of zsig63 protein activity. Zsig63 has antimicrobial
 CC activity and since exhibits high expression in salivary gland, can be
 CC used for treating dental caries, periodontal disease, thrush, and
 CC gastrointestinal disease, urinary tract infections, vaginal infections,
 CC skin infections and other epithelial wounds. The polypeptides can be
 CC used to establish normal microflora and protect against pathogenic
 CC colonization and invasion. Zsig63 can also be used for providing
 CC pro-inflammatory activity for treating chronic, tissue damage
 CC particularly in areas having limited or damaged vascular system, e.g.
 CC in diabetes, and for treating immunocompromised AIDS patients or in
 CC individuals that have undergone chemotherapy, radiation treatment, for
 CC treating lung infections e.g. in cystic fibrosis. Detection of zsig63
 CC polypeptide at relatively high levels in the trachea may indicate that
 CC such polypeptides may serve as a marker of lung dysfunction. Zsig63 is
 CC also useful in diagnosing conditions associated with salivary gland or
 CC lung dysfunction including salivary gland carcinoma, Pneumocystis carinii
 CC infection, emphysema, chronic bronchitis, prostate dysfunctions such
 CC as prostate adenocarcinoma, aiding digestion, and as components of
 CC defined cell culture media and may be used to replace serum that is
 CC commonly used in culture. The DNA is useful in gene therapy applications
 CC to increase or inhibit zsig63 activity, and for detecting abnormalities
 CC on human chromosome 4 (e.g. 4q12-4q13, associated with dentinogenesis
 CC imperfecta, and dentin dysplasia type II). Zsig63 is an adhesin family

CC member. The present sequence encodes human zsig63.
 XX
 SQ Sequence 1008 BP; 257 A; 251 C; 193 G; 307 T; 0 other;
 Query Match 100.0%; Score 1008; DB 25; Length 1008;
 Best Local Similarity 100.0%; Pred. No. 3.5e-207;
 Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 AGACGACGCTAAAAAGCCATGATCTTCTGCTCTTAAAGAAAGAAATATATTT 60
 1 AGACGACGCTAAAAAGCCATGATCTTCTGCTCTTAAAGAAAGAAATATATTT 60
 61 TAAAAATACATGCGGATTTTCTAAAAACAATATATATAGTTATATATAGAGTC 120
 61 TAAAAATACATGCGGATTTTCTAAAAACAATATATATAGTTATATATAGAGTC 120
 121 AATCAAAATGAAGCTTCTCTTGGGCGCTGATGTATGTGCTTTTGCAGAGAAAG 180
 121 AATCAAAATGAAGCTTCTCTTGGGCGCTGATGTATGTGCTTTTGCAGAGAAAG 180
 181 ACGGTTCCCTTCATTTGGTGAAGATGACAAATGACATGTCACCACTTCATCTCT 240
 181 ACGGTTCCCTTCATTTGGTGAAGATGACAAATGACATGTCACCACTTCATCTCT 240
 241 GAATATTCCTTATGGCAATCGGAATTTACCACTCTCTTTATATCGCCAGTGAATAC 300
 241 GAATATTCCTTATGGCAATCGGAATTTACCACTCTCTTTATATCGCCAGTGAATAC 300
 301 AGTCCCAAGTTACCTTGGAATATCTTACATGACACAGGGTTACCTTCATCTCTGAT 360
 301 AGTCCCAAGTTACCTTGGAATATCTTACATGACACAGGGTTACCTTCATCTCTGAT 360
 361 TCTAATCTCTCGGATTCCTCTGATTCCTCTGATTCCTCTGATTCCTCTGATTCCT 420
 361 TCTAATCTCTCGGATTCCTCTGATTCCTCTGATTCCTCTGATTCCTCTGATTCCT 420
 421 GTTGAATGTCCT 480
 421 GTTGAATGTCCT 480
 481 TTCAGCAGCTGACGACACCCGCTGCCACCTATTCAGCTGAGCTGCTGACCTGACCC 540
 481 TTCAGCAGCTGACGACACCCGCTGCCACCTATTCAGCTGAGCTGCTGACCTGACCC 540
 541 TCTTACAGCCACCTGTAGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 600
 541 TCTTACAGCCACCTGTAGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 600
 601 TCTCTGACAGGACACCTGTGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 660
 601 TCTCTGACAGGACACCTGTGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 660
 661 TCTCTGACAGGACACCTGTGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 720
 661 TCTCTGACAGGACACCTGTGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 720
 721 TCTCTGACAGGACACCTGTGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 780
 721 TCTCTGACAGGACACCTGTGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 780
 781 TCAAGTGAATTTCTCTAGAGAGTACATGAGTTCTATATATATATATATATATAT 840
 781 TCAAGTGAATTTCTCTAGAGAGTACATGAGTTCTATATATATATATATATATAT 840
 841 GAAATCTTACAAAAGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 900
 841 GAAATCTTACAAAAGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 900
 901 ATTCAATCTACATGATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 960
 901 ATTCAATCTACATGATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 960
 961 AAAAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1008


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FT      /tag= a
FT      /product= "secreted protein clone cp116 1"
XX      MO9901466-A1.
XX      14-JAN-1999.
XX      01-JUL-1998; 98WO-US13813.
XX      27-OCT-1997; 97US-0958304.
XX      02-JUL-1997; 97US-0887195.
XX      (GENY ) GENETICS INST INC.
XX      Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Racie LA;
XX      Spaulding V, Treacy M;
XX      WPI; 1999-105994/09.
XX      P-PSDB; AAW30653.
XX      New polynucleotides encoding secreted human proteins - are derived
XX      from human foetal brain, adult testes, adult brain, foetal kidney,
XX      adult salivary gland, or adult blood cDNA libraries, useful as, e.g.
XX      potential vaccines
XX      Claim 23; Page 70-71; 107bp; English.
XX      The present sequence encodes a human secreted protein from clone
XX      CP116 1, deposited as ATCC 98482. Human secreted protein clone
XX      polynucleotides and proteins are predicted to have biological
XX      activities which would make them suitable for treating, preventing or
XX      ameliorating medical conditions in humans and animals. Suggested
XX      activities include nutritional activity, cytokine and cell
XX      proliferation/differentiation activity, immune stimulating (e.g. as
XX      vaccines) or suppressing activity, haematopoiesis regulating activity,
XX      tissue growth activity, activin/inhibin activity, chemotactic/
XX      chemokinetic activity, haemostatic and thrombolytic activity, receptor/
XX      ligand activity, anti-inflammatory activity, cadherin/tumour invasion
XX      suppressor activity, and tumour inhibition activity. The polynucleotides
XX      are also stated to be useful for gene therapy.
XX      Sequence 1325 BP; 407 A; 289 C; 241 G; 388 T; 0 other;
XX
XX      Query Match 97.4%; Score 981.6; DB 20; Length 1325;
XX      Best Local Similarity 99.5%; Pred. No.1.9e-201;
XX      Matches 995; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
XX
XX      10 AAAAAAGCCATGATTTCTTCTGTTCTCTTAAAGAGAGAAAAATTAATTAATAATAC 69
XX      |||||||
XX      9 AAAAAAGCCATGATTTCTTCTGTTCTCTTAAAGAGAGAAAAATTAATTAATAATAC 68
XX      |||||||
XX      70 ATGCGGATTTCTTAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 129
XX      |||||||
XX      69 ATGCGGATTTCTTAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 128
XX      |||||||
XX      130 GAAGCTTCTCTTGGGCTGATTTGATGTTGTTTGAAGAGAGAGAGAGAGAGAGAGAG 189
XX      |||||||
XX      129 GAAGCTTCTCTTGGGCTGATTTGATGTTGTTTGAAGAGAGAGAGAGAGAGAGAGAG 188
XX      |||||||
XX      190 CTTCATTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 249
XX      |||||||
XX      189 CTTCATTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 248
XX      |||||||
XX      250 TTATGGCATCGGAATTTACACCTCTTTTATTAATTCGCGAGTGAATCACTCCCGAG 309
XX      |||||||
XX      249 TTATGGCATCGGAATTTACACCTCTCTTTATTAATTCGCGAGTGAATCACTCCCGAG 308
XX      |||||||
XX      310 TTACCTGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 369
XX      |||||||
XX      309 TTACCTGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 368
XX      |||||||
XX      370 TCCGTGATTTCCCTATGTCATCAATCCCTGTTTCCCTTGAATCACTGATTAATGT 429
XX      |||||||

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DB      369 TCCGTGATTTCCCTATGTCATCAATCCCTGTTTCCCTTGAATCACTGATTAATGT 428
XX      |||||||
XX      430 TCCGTGATTTCCCTATGTCATCAATCCCTGTTTCCCTTGAATCACTGATTAATGT 429
XX      |||||||
XX      429 TCCGTGATTTCCCTATGTCATCAATCCCTGTTTCCCTTGAATCACTGATTAATGT 428
XX      |||||||
XX      490 TGCAGACCCGCTGCCCCACTATTGACAGCTGAGCTGTCAGCTGCACTTTACAGC 549
XX      |||||||
XX      489 TGCAGACCCGCTGCCCCACTATTGACAGCTGAGCTGTCAGCTGCACTTTACAGC 548
XX      |||||||
XX      550 CACACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 609
XX      |||||||
XX      549 CACACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 608
XX      |||||||
XX      610 GGCACCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 669
XX      |||||||
XX      609 GGCACCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 668
XX      |||||||
XX      670 GGCACCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 729
XX      |||||||
XX      669 GGCACCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 728
XX      |||||||
XX      730 CAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 789
XX      |||||||
XX      729 CAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 788
XX      |||||||
XX      790 TTCTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 849
XX      |||||||
XX      789 TTCTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 848
XX      |||||||
XX      850 AAAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 909
XX      |||||||
XX      849 AAAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 908
XX      |||||||
XX      910 ACTACATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 968
XX      |||||||
XX      909 ACTACATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 967
XX      |||||||
XX      969 TGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1008
XX      |||||||
XX      968 TGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1007
XX      |||||||
XX
XX      RESULT 7
XX      AAX61352
XX      ID AAX61352 standard; cDNA; 959 BP.
XX
XX      AAX61352;
XX      14-JUL-1999 (first entry)
XX
XX      DE DNA encoding a human secreted protein.
XX
XX      Human secreted protein; cancer; tumour; neurodegenerative disorder;
XX      developmental abnormality; fetal deficiency; blood disorder; leukemia;
XX      immune system disease; autoimmune disease; hepatic disease;
XX      renal disease; lymphoma; inflammation; allergy; ischemic shock;
XX      Alzheimer's; cognitive disorder; schizophrenia; prostate disease;
XX      obesity; osteoclast; osteoporosis; arthritis; malignancy; testes disease;
XX      lung disease; thymus disease; digestive disorder; endocrine disorder;
XX      infection; AIDS; ss.
XX
XX      Homo sapiens.
XX      MO9922243-A1.
XX      06-MAY-1999.
XX      23-OCT-1998; 98WO-US22376.
XX      24-OCT-1997; 97US-0063387.
XX      24-OCT-1997; 97US-0062784.
XX      24-OCT-1997; 97US-0063088.

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PS Claim 4; Page 28-29; 33pp; English.

XX The present invention relates to a new secreted salivary protein, zslg63.
 CC The invention is useful for detecting in a test sample, the presence of
 CC an antagonist or agonist of zslg63 protein activity. The invention is
 CC also useful as an immunogen for producing an antibody to zslg63
 CC polypeptide. zslg63-cytokine fusion proteins or antibody-cytokine fusion
 CC proteins are useful for enhancing in vivo killing of target tissues.
 CC Pharmaceutical composition comprising purified zslg63 polypeptide are
 CC useful in the treatment of conditions associated with pathological
 CC microbes, including bacterial, fungal and viral infections. High
 CC expression of zslg63 in salivary gland suggests that anti-microbial
 CC polypeptides are useful for treatment of dental caries (tooth decay),
 CC periodontal disease, thrush and gastrointestinal disease. Other
 CC applications can be used in urinary tract infections, vaginal infections,
 CC prevention of infection in skin and other epithelial wounds. The
 CC polypeptides can be used to establish normal microflora and protect
 CC against pathogenic colonization and invasion. The invention is useful
 CC when pro-inflammatory activity is desired. Applications for
 CC such pro-inflammatory activity include the treatment of chronic tissue
 CC damage, particularly in areas having a limited or damaged vascular system
 CC e.g., damage in extremities associated with diabetes. Antagonists to
 CC zslg63 polypeptides may be useful as anti-inflammatory agents. The
 CC immune system is useful for the treatment of patients having incompetent
 CC or individuals that have undergone chemotherapy, radiation treatment. The
 CC invention is also useful for the treatment of lung infections associated
 CC with cystic fibrosis and its agonists or antagonists are useful for
 CC aiding digestion. The present nucleic acid sequence encodes the human
 CC secreted salivary protein zslg63 of the invention.

XX Sequence 657 BP; 72 A; 150 C; 114 G; 65 T; 256 other;

Query Match 45.6%; Score 460; DB 24; Length 657;

Best Local Similarity 61.0%; Pred. No. 2.2e-89;

Matches 401; Conservative 103; Mismatches 153; Indels 0; Gaps 0;

QY 128 ATGAAGCTTCTGCTGGGCTGATGATGCTTTGCAAGAAGAGCGTTC 187
 DB 1 ATGAATYTYNTVNTGGGCTGATGATGCTTTGCAAGAAGAGCGTTC 60
 QY 188 CCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 247
 DB 61 CCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 QY 248 CCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 307
 DB 121 CCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 QY 308 AGTTACCTGGAATATCTTACCTGATGATGATGATGATGATGATGATGAT 367
 DB 181 WMTATACCGNAGNAAATATATACGATGATGATGATGATGATGATGATGAT 240
 QY 368 TCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 427
 DB 241 WSNCCGAGTTCCTTATGATGATGATGATGATGATGATGATGATGATGAT 300
 QY 428 GTTCT 487
 DB 301 GTTCT 360
 QY 488 GCTGAGAGACCCGCTGCTGCTGATGATGATGATGATGATGATGATGAT 547
 DB 361 GCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGN 420
 QY 548 GCGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 607
 DB 421 GCGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 608 GAGGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
 DB 481 GAGGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 540

QY 668 GAGGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 727
 DB 541 GAGGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 QY 728 GCGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 784
 DB 601 GCGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 657

RESULT 10

AAS20592
 ID AAS20592 standard; cDNA; 657 BP.

AC AAS20592;

DT 23-APR-2002 (first entry)

DE Human zslg63 degenerate cDNA coding sequence.

KW Human; zslg63; chromosome 4q12-q13; salivary protein; antimicrobial; ss;
 KW microbial infection; tooth decay; periodontal disease; thrush; emphysema;
 KW gastrointestinal disease; urinary tract infection; vaginal infection;
 KW skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;
 KW acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;
 KW chronic bronchitis; gene therapy; protein therapy; gene.

OS Homo sapiens.

PN US6311413-B1.

PD 18-DEC-2001.

PF 17-MAR-2000; 2000US-0527345.

PR 17-MAR-1999; 99US-124820P.

PA (ZYMO) ZYMOGENETICS INC.

PI Adler DA, Sheppard PO;

PT WPI; 2002-096707/13.

PS Claim 3; Column 51-52; 29pp; English.

CC The invention relates to a polynucleotide derived from the 4q12-q13
 CC region of human chromosome 4 and encoding a zslg63 polypeptide, a
 CC secreted salivary protein with anti-microbial activity. Due to their
 CC microbial activity, the sequences can be used in the study of microbial
 CC infections, e.g., for recombinant production of anti-microbial proteins.
 CC The sequences can be used in the treatment of tooth decay, periodontal
 CC disease, thrush, gastrointestinal disease, urinary tract infections,
 CC vaginal infections, skin infections, epithelial wounds, chronic tissue
 CC damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung
 CC infections, sarcoidosis, emphysema and chronic bronchitis. This sequence
 CC represents a degenerate cDNA encoding human zslg63.

XX Sequence 657 BP; 72 A; 150 C; 114 G; 65 T; 256 other;

Query Match 45.6%; Score 460; DB 24; Length 657;

Best Local Similarity 61.0%; Pred. No. 2.2e-89;

Matches 401; Conservative 103; Mismatches 153; Indels 0; Gaps 0;

QY 128 ATGAAGCTTCTGCTGGGCTGATGATGCTTTGCAAGAAGAGCGTTC 187
 DB 1 ATGAATYTYNTVNTGGGCTGATGATGCTTTGCAAGAAGAGCGTTC 60
 QY 188 CCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 247
 DB 61 CCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120

QY 248 CCTATGCAATACGGAATTACCACTCTCTTATATGCCCCAGTACAGTCCCC 307.
 DB 121 CCAATGAGNATMGNAAYTTCNCNCNCTTATATATGACNCTGNAAYCNCNCN 180
 QY 308 AGTTACCCCTGGGAATCTTACACTGACAGGGTTACCTTCGATCCCTGGAATCTTA 367
 DB 181 WNTATCCNGNNAAYACNTATACGAYACNGAYTTCNCNMSNTATYCCNTGATHTYNA 240
 QY 368 TCTCCTGATTCCTCCATGCTATACATCCGATGTTTCCCTAGCTACTAGTGAAT 427
 DB 241 WNCNCGNATTCNTATAGTNTATYCAATHTMGNGATTCNTATGACNACNARNTNAY 300
 QY 428 GTTCTCTCTCCCTCTTACAGGGGTTTCCGTTTTCCTCTTCAAGGTTTTTTTCAG 487
 DB 301 GTTNCNCCNCTTCNCNCNMGNGATTCNTATGTCNCNCNMSNTATYTTTTCN 360
 QY 488 GGTGACGACCCGCTGCCCCCACTATTTGACGCTGACCTGCTGACCTCTTA 547
 DB 361 GCGNCGNCCNCGNCCNCCNATHTGNCNCGNCGNCCNCGNCCNCTNACN 420
 QY 548 GCCACACCTGTAGACGCTGAGCTGTGACAGGGGCCCCCTGTGACGCTGAGCTG 607
 DB 421 GCGNCCNCGNCCNCGNCCNCGNCCNCGNCCNCGNCCNCGNCCNCGNCCN 480
 QY 608 GAGGACCTGTGAGCTGAGCTGTGACAGGACCTGTGACGCTGAGCTGCTG 667
 DB 481 GARGCNCNCTGNCNCGNCCNCGNCCNCGNCCNCGNCCNCGNCCNCGNCCN 540
 QY 668 GAGGACCTGTGAGCTGAGCTGAGCTGAGGAACTTACACGCTGAGCTGCTG 727
 DB 541 GARGCNCNCTGNCNCGNCCNCGNCCNCGNCCNCGNCCNCGNCCNCGNCCN 600
 QY 728 GCCAAGCTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 784
 DB 601 GCGNCCNCGNCCNCGNCCNCGNCCNCGNCCNCGNCCNCGNCCNCGNCCN 657

RESULT 11
 ABX93595
 ID ABX93595 standard; DNA; 657 BP.
 XX
 AC ABX93595;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE Human zslg63 degenerate sequence.
 XX
 XX de; zslg63; adhesin; salivary gland; dental carrier;
 KM periodontal disease; thrush; gastrointestinal disease; epithelial wound;
 KM urinary tract infection; vaginal infection; skin infection;
 KM pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS;
 KM lung infection; cystic fibrosis; lung dysfunction; digestive;
 KM salivary gland carcinoma; Pneumocystis carinii infection; emphysema;
 KM chronic bronchitis; prostate dysfunction; prostate adenocarcinoma;
 KM cell culture media; gene therapy; human chromosome 4q12-4q13;
 KM dentinogenesis imperfecta; dentin dysplasia type II.
 OS Synthetic.
 XX
 PN US2002173027-A1.
 XX
 PD 21-NOV-2002.
 XX
 PF 03-AUG-2001; 2001US-0922469.
 XX
 PR 17-MAR-1999; 99US-124820P.
 PR 17-MAR-2000; 2000US-0527345.
 XX
 PA (ADLER/) ADLER D A.
 PA (SHEP/) SHEPPARD P O.
 XX
 PI Adler DA, Sheppard PO;

DR WP1; 2003-328428/31.
 XX
 PT Novel isolated zslg63 polypeptide, member of the adhesin family, useful
 PT for treating dental carrier, periodontal disease, thrush,
 PT gastrointestinal disease, urinary tract infections, vaginal infections,
 PT skin infections
 PS
 PS Claim 4; Page 28; 32pp; English.
 CC The invention relates to an isolated zslg63 polypeptide comprising at
 CC least 90% identity to an amino acid sequence which comprises domain 1 of
 CC zslg63, domain 2, domain 3, mature zslg63 and full length zslg63. Also
 CC included are the polynucleotide encoding zslg63, a zslg63 expression
 CC vector, a cultured cell comprising the vector and expressing the protein,
 CC a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37,
 CC 38-126, 127-219 or 16-219 of zslg63 and an additional protein), using a
 CC zslg63 reporter gene construct to identify zslg63 agonists, and
 CC producing an anti-zslg63 antibody using zslg63 immunogenic peptides,
 CC antagonist of zslg63 protein activity. Zslg63 has antimicrobial
 CC activity and since exhibits high expression in salivary gland, can be
 CC used for treating dental carrier, periodontal disease, thrush, and
 CC gastrointestinal disease, urinary tract infections, vaginal infections,
 CC skin infections and other epithelial wounds. The polypeptides can be
 CC used to establish normal microflora and protect against pathogenic
 CC pro-inflammatory activity for treating chronic, tissue damage
 CC particularly in areas having limited or damaged vascular system, e.g.
 CC in diabetes, and for treating immunocompromised AIDS patients or in
 CC individuals that have undergone chemotherapy, radiation treatment, for
 CC treating lung infections e.g. in cystic fibrosis. Detection of zslg63
 CC polypeptide at relatively high levels in the trachea may indicate that
 CC such polypeptides may serve as a marker of lung dysfunction. Zslg63 is
 CC also useful in diagnosing conditions associated with salivary gland or
 CC lung dysfunction including salivary gland carcinoma, Pneumocystis carinii
 CC infection, emphysema, chronic bronchitis, prostate dysfunctions such
 CC as prostate adenocarcinoma, aiding digestion, and as components of
 CC defined cell culture media and may be used to replace serum that is
 CC commonly used in culture. The DNA is useful in gene therapy applications
 CC to increase or inhibit zslg63 activity, and for detecting abnormalities
 CC on human chromosome 4 (e.g. 4q12-4q13), associated with dentinogenesis
 CC imperfecta, and dentin dysplasia type II). Zslg63 is an adhesin family
 CC member. The present sequence represents all possible sequences that
 CC may encode zslg63.
 CC
 CC Sequence 657 BP; 72 A; 150 C; 114 G; 65 T; 256 other;
 SQ
 Query Match 45.6%; Score 460; DB 25; Length 657;
 Best Local Similarity 61.0%; Pred. No. 2,2e-89;
 Matches 401; Conservative 103; Mismatches 153; Indels 0; Gaps 0;
 QY 128 ATGAAGCTTCTCCCTTGGGCGCGCATTTGATGTGCTTTGAGAGAGAGACGGTTC 187
 DB 1 ATGAARATYNTYNTTGGGCGCTGATGATGNTGTGNCCTTTGCMNNAARNGNNTTY 60
 QY 188 CCGTTCATTTGAGATGACATGACATGCTGACCCCATTCATCATCTCTGATATT 247
 DB 61 CCGTTATHTGGGAGAGAYAAVAGAYGNCAYCCNTYTCAICCMWSNTNNAAYTH 120
 QY 248 CCTATGCAATGGAATTTACACCTCTCTTTATTTATCCCGCATGATCACTGCC 307
 DB 121 CCAATGAGNATMGNAAYTTCNCNCNCTTATATATGACNCTGNAAYCNCNCN 180
 QY 308 AGTTACCCCTGGGAATCTTACACTGACAGGGTTACCTTCGATCCCTGGAATCTTA 367
 DB 181 WNTATCCNGNNAAYACNTATACGAYACNGAYTTCNCNMSNTATYCCNTGATHTYNA 240
 QY 368 TCTCCTGATTCCTCCATGCTATACATCCGATGTTTCCCTAGCTACTAGTGAAT 427
 DB 241 WNCNCGNATTCNTATAGTNTATYCAATHTMGNGATTCNTATGACNACNARNTNAY 300
 QY 428 GTTCTCTCTCCCTCTTACAGGGGTTTCCGTTTTCCTCTTCAAGGTTTTTTTCAG 487

Db 301 GTNCCNCTNTCCNCCNMGNGNTTTCNTTGTTCNCCNMSNMGNTTTCNCCN 360
 QY 488 GCTGAGACCCGCTGCCCCACCTATTGAGCTGAGCTGAGCTGACCTCTTACA 547
 Db 351 GNGGNGCNCNGCNGCNCNGCNCNAHGCNGNGARCCNGCNGCNGCNCNTTACN 420
 QY 548 GCCACACCTGTAGACCTGAGCTGAGCTGAGGAGGCCCCCTGTTCGAGCTGAGCTGCTCA 607
 Db 421 GGNACNCCNGTNGCNGCNGARCCNCCNCGNCGNCGTNGCNGCNGARCCNCCN 480
 QY 608 GAGGACCTGTGTGAGCTGAGCTGCTGCAAGGCACTGTTCGAGCTGAGCTGCTGCA 667
 Db 481 GARGCNCNGTNGCNGCNGARCCNCCNCGNCGNCGTNGCNGCNGARCCNCCN 540
 QY 668 GAGGACCTGTGTGAGCTGAGCTGCTGCAAGGCACTGTTCGAGCTGAGCTGCTCA 727
 Db 541 GARGCNCNGTNGCNGCNGARCCNCCNCGNCGNCGTNGCNGCNGARCCNCCN 600
 QY 728 GCCAAGCTGTGCTGCCCCAGAACCTGACCTTCTCCCTCTTGAACAGCAATGAG 784
 Db 601 GCNAARCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 657

RESULT 12

AAV89597 standard; cDNA; 470 BP.

AAV89597;

15-FEB-1999 (first entry)

EST clone CP251.

Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemokinesis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour; gene therapy; ss.

Homo sapiens.

MO9845436-A2.

15-OCT-1998.

10-APR-1998; 98WO-US06955.

10-APR-1997; 97US-0838821.

(GENE) GENETICS INST INC.

Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D; Racie LA, Spaulding V, Treacy M; WPI, 1999-070077/06.

New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.

Claim 1; Page 269; 618pp; English.

The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy.

XX Sequence 470 BP; 116 A; 115 C; 83 G; 156 T; 0 other;

Query Match 44.5%; Score 449; DB 20; Length 470;

Best Local Similarity 98.9%; Pred. No. 4.5e-87;

Matches 452; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 11 AAAAGCATATATCTTCTGTTCTCTCTTAAAGAAAGAAATATATATTAATCA 70
 Db 11 AAGAGCTAGTATCTTCTGTTCTCTCTTAAAGAAAGAAATATATTAATCA 70
 QY 71 TTGGGATTTTCTTAAACAAATTAATTAAGTTAATTAATTAATTAATTAATTA 130
 Db 71 TTGGGATTTTCTTAAACAAATTAATTAAGTTAATTAATTAATTAATTAATTA 130
 QY 131 AAGCTTCTCTTGGGCTGATGTAATGTTATGTTATGTTATGTTATGTTATGTT 190
 Db 131 AAGCTTCTCTTGGGCTGATGTAATGTTATGTTATGTTATGTTATGTTATGTT 190
 QY 191 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 250
 Db 191 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 250
 QY 251 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 310
 Db 251 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 310
 QY 311 TACCTGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 370
 Db 311 TACCTGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 370
 QY 371 CCTGATTTCCCTTATGTCATGATGATGATGATGATGATGATGATGATGATGAT 430
 Db 371 CCTGATTTCCCTTATGTCATGATGATGATGATGATGATGATGATGATGATGAT 430
 QY 431 CCT 467
 Db 431 CCT 467

RESULT 13

AAV89646 standard; cDNA; 450 BP.

AAV89646;

15-FEB-1999 (first entry)

EST clone CP116.

Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemokinesis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour; gene therapy; ss.

Homo sapiens.

MO9845436-A2.

15-OCT-1998.

10-APR-1998; 98WO-US06955.

10-APR-1997; 97US-0838821.

(GENE) GENETICS INST INC.

Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D; Racie LA, Spaulding V, Treacy M; WPI, 1999-070077/06.

New polynucleotides encoding human secreted proteins - derived from

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 16, 2004, 07:23:58 ; Search time 89 Seconds
(without alignments)
4999.036 Million cell updates/sec

Title: US-09-923-236-1

Perfect score: 1008

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Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	460	45.6	657	US-09-527-345-3	Sequence 3, Appli
3	121.2	12.0	3489	US-08-728-323A-1	Sequence 1, Appli
4	121.2	12.0	3489	US-09-298-568-1	Sequence 1, Appli
5	121.2	12.0	3489	US-09-410-399-1	Sequence 1, Appli
6	121.2	12.0	32207	US-08-770-379-20	Sequence 20, Appli
7	121.2	12.0	32207	US-08-757-669A-20	Sequence 20, Appli
8	121.2	12.0	32207	US-09-230-371A-20	Sequence 20, Appli
9	100	9.9	1037	US-09-181-585-3	Sequence 3, Appli
10	100	9.9	1159	US-09-181-585-1	Sequence 1, Appli
11	100	9.9	1471	US-09-181-585-2	Sequence 2, Appli
12	93.6	9.3	397	US-09-253-691-3	Sequence 3, Appli
13	92	9.1	543	5273901-6	Patent No. 5273901
14	87.6	8.7	234	US-08-469-802B-3	Sequence 3, Appli
15	87.6	8.7	234	US-08-267-803B-3	Sequence 3, Appli
16	86.6	8.6	786	US-08-403-379A-2	Sequence 2, Appli
17	86.6	8.6	786	US-08-929-414-2	Sequence 2, Appli
18	85.2	8.5	1926	US-09-249-585A-2	Sequence 2, Appli
19	85.2	8.5	1926	US-09-410-399-3	Sequence 3, Appli
20	85.2	8.5	2580	US-09-050-863-2	Sequence 2, Appli
21	85.2	8.5	2580	US-09-359-081-2	Sequence 2, Appli
22	85.2	8.5	5452	US-09-130-114-1	Sequence 1, Appli
23	85.2	8.5	8705	US-09-647-344A-14	Sequence 14, Appli
24	85.2	8.5	9600	US-08-910-647-1	Sequence 1, Appli
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C 35	83.6	8.3	477	4	US-09-135-994-1	Sequence 1, Appli
C 36	83.6	8.3	477	4	US-09-684-843A-1	Sequence 1, Appli
C 37	83.2	8.3	397	4	US-09-253-691-3	Sequence 1, Appli
C 38	83	8.2	2830	2	US-09-010-928B-1	Sequence 1, Appli
C 39	80	7.9	533	6	5482709-5	Patent No. 5482709
C 40	78.2	7.8	16442	3	US-08-781-891-208	Sequence 208, App
C 41	78.2	7.8	16442	4	US-09-618-166-208	Sequence 7, Appli
C 42	77.8	7.7	203	3	US-09-043-303-7	Sequence 2, Appli
C 43	77.2	7.7	2824	2	US-09-010-928B-3	Sequence 3, Appli
C 44	75.8	7.5	195	1	US-08-469-802B-2	Sequence 2, Appli
C 45	75.8	7.5	195	2	US-08-267-803B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1						
US-09-527-345-1						
; Sequence 1, Application US/09527345						
; Patent No. 6331413						
; GENERAL INFORMATION:						
; APPLICANT: Sheppard, Paul O.						
; TITLE OF INVENTION: ADLER, David A.						
; FILE REFERENCE: 97-71						
; CURRENT APPLICATION NUMBER: US/09/527,345						
; PRIOR APPLICATION NUMBER: 1999-03-17						
; PRIOR FILING DATE: 1999-03-17						
; NUMBER OF SEQ ID NOS: 9						
; SOFTWARE: FastSeq for Windows Version 3.0						
; SEQ ID NO 1						
; LENGTH: 1008						
; TYPE: DNA						
; ORGANISM: Homo sapiens						
; FEATURE:						
; NAME/KEY: CDS						
; LOCATION: (128)...(784)						
US-09-527-345-1						
Query Match						
Best Local Similarity 100.0%; Pred. No. 2,7e-234;						
Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
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DB	61	TAAATATACATGCGATTTCTTAAACATTAATTAATTAATTAATTAAT	120			
QY	121	AATCAATGAGAGCTTCTTGGCGCTGATGATGATGATGATGATGATGAT	180			
DB	121	AATCAATGAGAGCTTCTTGGCGCTGATGATGATGATGATGATGATGAT	180			
QY	181	ACGTTCCCTTATGATGATGATGATGATGATGATGATGATGATGATGAT	240			
DB	181	ACGTTCCCTTATGATGATGATGATGATGATGATGATGATGATGATGAT	240			
QY	241	GAATATCTTATGATGATGATGATGATGATGATGATGATGATGATGAT	300			
DB	241	GAATATCTTATGATGATGATGATGATGATGATGATGATGATGATGAT	300			
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Oy		361	TCTAATCTTCTCTGGATTTCCCCTAATGTCTATCATCANTCCGGTGTTTTCCCTTAGCTACTCA	420
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Oy		421	GTTGAATGTTCTCTCTCTCCCTCTAGAGGGGTTTCCCGTTTGTGCCCTCTCAAGGTTTTT	480
Db		421	GTTGAATGTTCTCTCTCTCTCCCTCTAGAGGGGTTTCCCGTTTGTGCCCTCTCAAGGTTTTT	480
Oy		481	TTTGACAGCTGCAGCACCCCGCTGCCACCACCTAATTGACGTGAGCCCTGCTGACGCTCACCC	540
Db		481	TTTGACAGCTGCAGCACCCCGCTGCCACCACCTAATTGACGTGAGCCCTGCTGACGCTCACCC	540
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Oy		661	TGCTGCAGAGGGACCTGTTGGAAGCTGAGGCCTGCTGCAGAGGGAACCTTTCACAGCTAGGCC	720
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Oy		901	ATTCAATCTCACTACATNTGATTTGTTTGTGTGTAGT TTTTCTTGAGCTTAATTAATTAATGGA	960
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RESULT 2				
US-09-527-345-3				
; Sequence 3, Application US/09527345				
; Patent No. 6331413				
; GENERAL INFORMATION:				
; APPLICANT: Sheppard, Paul O.				
; APPLICANT: Adler, David A.				
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE				
; FILE REFERENCE: 97-71				
; CURRENT APPLICATION NUMBER: US/09/527,345				
; PRIOR FILING DATE: 1999-03-17				
; PRIOR APPLICATION NUMBER: US 60/124,820				
; NUMBER OF SEQ ID NOS: 9				
; SOFTWARE: FastSeq for Windows Version 3.0				
SEQ ID NO 3				
LENGTH: 657				
TYPE: DNA				
ORGANISM: Artificial Sequence				
FEATURES:				
OTHER INFORMATION: Degenerate polynucleotide sequence for zsig63				
NAME/KEY: misc_feature				
LOCATION: (1)...(657)				
OTHER INFORMATION: n = A,T,C or G				
US-09-527-345-3				

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Query Match          45.6%; Score 460; DB 4; Length 657;
Beet Local Similarity 61.0%; Pred. No.5,6e-102;
Matches 401; Conservative 103; Mismatches 153; Indels 0; Gaps 0

QY      128 ATGAAGCTTCTCTTTG6GCGTCATGTATGTGTGTGCTTTTGCAAGAAGAGACGGTTC
DB      1   ATGAATATNTYNTYNTYG6GCGTGTATHTGTTGYGTNGCNTTYTGCMGNNAABMGNNGNTTY
QY      188 CCGTTCATTGGTGAAGATGACAATGACATGGTCAACCACCTTCATCCACTCTGTAATAT
DB      61  CCNTTAAHGNNGARGAAYAAAGAYAGGNCAYCCNYTNCAACCMBSNTNNAAYAH
QY      248 CCTATGCGCATACGGAATTTTACCAACCTCCTCTTTTATTCGCCACAGTAATACAGTCCC
DB      121 CCNTATYGNNAATHMGMAAYTTTCCNCCNCCNTTNTATYTAMGNCGNGTNAAYACNGTNCCN
QY      308 AGTTACCTTGGGAATACTTACACTGACACAGGGTTACTCTGTATCCTCGATTCTACT
DB      181 WSNATAYCCNGNNAAYACMTATAVACNGAYACNGSANTYNCCMSWTACATGTGATHTYTMACN
QY      368 TCTCCTGGAATCCCCCTATGTCTATCAACTCCGTGGTTCCTCCTTAGCTACTAGTTGAT
DB      241 WSNCCNGSNTTYCCNTATGINTATCAATHMNGSNTTYCCNYTNGCAACARITTAAY
QY      428 GTTCCTCTCTCCCTCTCTTGAAGGGTTCCTCCGTTTTGCCTCTCTCAAGTTTTTTTCAAGA
DB      301 GTNCCNCCNYTNCNCCMGANGNTTYCCNTTYGTNCCNCCMSWNTTYTTYWSNGCN
QY      488 GCTGACAGACCCGCTGCCCACTATTTGACACTGACCTGCTGACAGCTGCACCTCTTACA
DB      361 GCNCGNCCNGNCCNGCNCACNAHTGCNCGNARCCNGCNGCNGCNCNTTNAACN
QY      548 GCCAACACCTGTAGACAGCTGACCTGCTGCAAGGGCCCTCTGTGACGTAGAGCTCTGCA
DB      421 GCMAACNCCNGTNGCNGCNGARCCNGCNGCNGGANGCNGTNGCNGCNGARCCNGCNGCN
QY      608 GAGCACCTGTTGAGAGCTGAGCCTGCTGCAAGGACCTGTTGACAGCTGAGCCTCTGCA
DB      481 GARCCNCCNGTNGCNGCNGARCCNGCNGCNGARCCNCGTNGCNGCNGARCCNGCNGCN
QY      668 GAGCACCTGTTGAGAGCTGAGCCTGCAAGGAACTTGACACGCTGAGCCTCTGCA
DB      541 GARCCNCCNGTNGCNGCNGARCCNGCNGCNGARCCNMSNCCNGCNGARCCNGCNGCN
QY      728 GCCAAGCTCTGTGCCCCAGAACTCACCTTCTCTCTCTTGAACAGGCAAAATCAG
DB      601 GCNAARCCNGNCCNGCNGARCCNCAVCNMSNCCNMSNTYNGARCCNAAYCAR
RESULT 3
US-08-728-323A-1/c
Sequence 1, Application US/08728323A
Patent No. 5948676
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Encoding Same And Uses Thereof
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```

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1  OPERATING SYSTEM: PC-DOS/MS-DOS
2  SOFTWARE: PatentIn Release #1.0, Version #1.30
3  CURRENT APPLICATION DATA:
4  APPLICATION NUMBER: US/08/728,323A
5  FILING DATE:
6  CLASSIFICATION: 435
7  ATTORNEY/AGENT INFORMATION:
8  NAME: White, John P.
9  REGISTRATION NUMBER: 28,678
10 REFERENCE/DOCKET NUMBER: 05/5152268/JPM/MSC/SKS
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: 212-278-0400
13 TELEFAX: 212-391-0525
14 INFORMATION FOR SEQ ID NO: 1:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 3489 base pairs
17 TYPE: nucleic acid
18 STRANDEDNESS: single
19 TOPOLOGY: linear
20 MOLECULE TYPE: DNA (genomic)
21 FEATURE:
22 NAME/KEY: CDS
23 LOCATION: 1..3489
24 US-08-728-323A-1

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Query Match	12.0%	Score 121.2;	DB 2;	Length 3489;
Best Local Similarity	58.7%	Pred. No. 8.9e-20;		
Matches 210; Conservative	0;	Mismatches 148;	Indels 0;	Gaps 0

[illegible]

```

: RESULT 4
: US-09-298-568-1/c
: Sequence 1, Application US/09298568
: Patent No. 6322792
: GENERAL INFORMATION:
: APPLICANT: Kleif, Elliott D.
: APPLICANT: Ballestas, Mary E.
: APPLICANT: Kaye, Kenneth M.
: TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
: TITLE OF INVENTION: VIRUS DNA TO MEDIANE EFFICIENT EPISOME PERSISTENCE
: FILE REFERENCE: 16412-10001R
: CURRENT APPLICATION NUMBER: US/09/298,568
: CURRENT FILING DATE: 1999-04-21
: EARLIER APPLICATION NUMBER: US 60/109,422
: EARLIER FILING DATE: 1998-11-19
: NUMBER OF SEQ. ID NOS: 3
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 3489

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; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-1

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Query Match	12.0%	Score 121.2;	DB 4;	length 3489;
Best Local Similarity	58.7%	Pred. No. 8,9e-20;		
Matches 210; Conservative	0;	Mismatches 146;	Indels 0;	Gaps 0;

OY	413	GCTACTAGTTGAATGTTCTCCCTCCCTCCCTCCTAGAGGGATTTCCGGTTATGCCCTTTCA	472
Db	2188	GCTGCTCATCTGCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTGCTGCTCAT	21229
OY	473	AGGTTTTTTCAGCAGCTGACGACCCGCTGCCACCTATTCAGAGCTGAGCTGCTGCA	532
Db	2128	CTGCTGCTCTCTGCTCATCTGCTGCTCTGCTCATCTGCTGCTCATCTGCTGCT	20659
OY	533	GCTGCACCTCTTACAGGCACACCTGTATGACAGCTGAGCTGCTGACAGGGGCCCTGTTGCA	592
Db	2068	GCTCATCTCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTCATCTGCTGCT	20029
OY	593	GCTGAGCTTCTGTGAGGCACTGTTGAGCTGAGCTGCTGTGACAGGCACTGTTGCA	652
Db	2008	GCTCATCTCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTCATCTGCTGCT	19449
OY	653	GCTGAGGCTCTGTGACAGGCACTGTTGAGTGTGAGGCACTGTGACAGGAACTTACCA	712
Db	1948	GCTCATCTCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCT	18839
OY	713	GCTGAGGCTGTACAGGCAAGCTGCTGCTGCCGAAAGCTCAACCTTCTCCCTCTCTTG	770
Db	1888	GCTCATCTCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTCATCTGCTGCT	1831

```

RESULT 5
US-09-410-399-1/c
: Sequence 1, Application US/09410399
: Patent No. 6482587
: GENERAL INFORMATION:
: APPLICANT: Robertson, Erle S.
: APPLICANT: Colter, Murray A.
: TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
: TITLE OF INVENTION: to Genomic Host DNA
: FILE REFERENCE: UM-03778
: CURRENT APPLICATION NUMBER: US/09/410.399
: CURRENT FILING DATE: 1999-10-01
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 3489
: TYPE: DNA
: ORGANISM: Kapost's sarcoma-associated herpesvirus
: US-09-410-399-1

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	Query Match	Best Local Similarity	Score	IDB	Length
			12.0%;	4;	3489;
			58.7%;	8.9e-20;	
	Matches	Conservative	0;	Mismatches	Indels
QY	413	GCTACTCAGTGGATGTTCTCTCTCTCTCTAAGGGGTTCGCCGTTTGCCCTCTTCA	472		
Db	2188	GCTGCTCATCTCTGCTGCTGCATCCCTGCTGCTCTATCTCTGCTCCGCTCAT	2129		
QY	473	AGGTTTTTTCACAGCGTAGACACCAGCCCACTATTGACGCTGAAGCCGTGCA	532		
Db	2128	CCTGCTGCTCTGCTATCTGTGCTCTCTGCTCATCTGCTGCTTCACTCTGCTCT	2065		
QY	533	GCTGCACCTTTACAAGCACACCTGTAGACGTGAAGCTTCTGACGGGGCCCCCTGTTGA	592		
Db	2068	GCTCATCTCTGCTGCTCATCTGCTGCTCATCTCTGCTGCTCATCTGCTGCT	2009		
QY	593	GCTGAGCTGCTGCAGAAGCACTGTTGAGAGCTGAGCTGCTCAAGAGCAACCTGTTGA	652		
Db	2008	GCTCATCTGCTCTGCTCATCTGCTGCTGCTCATCTCTGCTGCTCATCTGCTGCT	1949		

QY 653 GCTGAGCCTGCTGACAGAGCACTGTTGAGTGGAGCCAGCTGACAGAGAACTTTCACCA 712
DB 1948 GCTCATCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTCATCTGCTGCTGCT 1889
QY 713 GCTGAGCCTGCTGACAGCCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
DB 1888 GCTCATCTGCTGCTGCTGCTCATCTGCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTGCT 1831

RESULT 6

US-08-770-379-20
; Sequence 20, Application US/08770379
; Patent No. 5849564
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
; TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770.379
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 52342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-770-379-20

Query Match 12.0%; Score 121.2; DB 2; Length 32207;
Best Local Similarity 58.7%; Pred. No. 2.6e-19;
Matches 210; Conservative 0; Mismatches 148; Indels 0; Gaps 0;
QY 413 GCTACTCAGTGAATGTTCA 472
DB 19809 GCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCAT 19868
QY 473 AGGTTTTTTCAGACAGCTGACACCCGCTGCCCCCACTATTGACAGCTGAGCTGCTGCA 532
DB 19869 CCGTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19928
QY 533 GCTGACCTCTTTACAGCCACACCTGTAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 592
DB 19929 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19988
QY 593 GCTGAGCCTGCTGACAGAGCACTGTTGAGTGGAGCCAGCCTGCTGCTGCTGCTGCTGCTGCA 652
DB 19989 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20048

QY 653 GCTGAGCCTGCTGACAGAGCACTGTTGAGTGGAGCCAGCCTGACAGAGAACTTTCACCA 712
DB 20049 GCTCATCTGCTGCTGCTGCTCATCTGCTGCTGCTGCTCATCTGCTGCTGCTGCTGCTGCT 20108
QY 713 GCTGAGCCTGCTGACAGCCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
DB 20109 GCTCATCTGCTGCTGCTGCTCATCTGCTGCTGCTGCTCATCTGCTGCTGCTGCTGCTGCTGCT 20166

RESULT 7

US-08-757-669A-20
; Sequence 20, Application US/08757669A
; Patent No. 6183751
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757.669A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45185-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-757-669A-20

Query Match 12.0%; Score 121.2; DB 3; Length 32207;
Best Local Similarity 58.7%; Pred. No. 2.6e-19;
Matches 210; Conservative 0; Mismatches 148; Indels 0; Gaps 0;
QY 413 GCTACTCAGTGAATGTTCA 472
DB 19809 GCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCAT 19868
QY 473 AGGTTTTTTCAGACAGCTGACACCCGCTGCCCCCACTATTGACAGCTGAGCTGCTGCA 532
DB 19869 CCGTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19928
QY 533 GCTGACCTCTTTACAGCCACACCTGTAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 592
DB 19929 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19988
QY 593 GCTGAGCCTGCTGACAGAGCACTGTTGAGTGGAGCCAGCCTGCTGCTGCTGCTGCTGCTGCA 652

Db 19889 GCTCATCTGCTGCTGCTCATCTGCTGCTCATCTGCTGCTCATCTGCTGCT 20048
Qy 653 GCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712
Db 20049 GCTCATCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTGCTGCTGCT 20108
Qy 713 GCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
Db 20109 GCTCATCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTGCTGCTGCTG 20166

RESULT 8
US-09-230-371A-20

; Sequence 20, Application US/09230371A
; Patent No. 6348586
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A
; APPLICANT: Russco, James J
; APPLICANT: Edelman, Isidore S
; APPLICANT: Moore, Patrick S
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
; FILE REFERENCE: 45185-G-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230,371A
; PRIOR FILING DATE: 1999-11-17
; PRIOR FILING DATE: 1997-07-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 20
; LENGTH: 32207
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-20

Query Match 12.0%; Score 121.2; DB 4; Length 32207;
Best Local Similarity 58.7%; Pred. No. 2,6e-19;
Matches 210; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

Qy 413 GCTACTCAGTTGATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 472
Db 19809 GCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19868
Qy 473 AGGTTTTTTCAGACAGTGCAGACCGCGTGGCCCACTTATGACGTGAGCGTGCAGCA 532
Db 19869 CCGTGGCTGCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19928
Qy 533 GCTGCACTCTTACAGCAACCTGTAGACGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCA 592
Db 19929 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19988
Qy 593 GCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 652
Db 19989 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20048
Qy 653 GCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712
Db 20049 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20108
Qy 713 GCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
Db 20109 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20166

RESULT 9
US-09-181-585-3

; Sequence 3, Application US/09181585
; Patent No. 6524791
; GENERAL INFORMATION:
; APPLICANT: Rannum, Laura P.W.
; APPLICANT: Koob, Michael
; TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION

; FILE REFERENCE: 1100900101
; CURRENT APPLICATION NUMBER: US/09/181,585
; CURRENT FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA
US-09-181-585-3

Query Match 9.9%; Score 100; DB 4; Length 1037;
Best Local Similarity 56.8%; Pred. No. 6.6e-15;
Matches 184; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

Qy 406 TCCCTTAGCTACTCAGTGAATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 465
Db 591 TTCCTTAGCTAGACCTGGGCTCTTATGTAAGAAACCTGGCTTACTACTACTACTAC 650
Qy 466 TCCCTTAGCTTTTTCAGACGCTGACAGACCGCTGCCCCACTATTGACGCTGAGCC 525
Db 651 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 710
Qy 526 TCCCTGAGCTGACCTCTTACAGCCACCTGTAGAGCTGAGCCGCTGACGGGCCCC 585
Db 711 TCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
Qy 586 TCTTGCAGCTGACCTGCTGACAGAGCACTGTGTGAGCTGACCTGCTGACAGACAC 645
Db 771 TCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 830
Qy 646 TCTTGCAGCTGACCTGCTGACAGAGCACTGTGTGAGCTGACCCGCTGACAGAGAAC 705
Db 831 TCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 890
Qy 706 TTCACAGCTGAGCCGTGTACAGC 729
Db 891 TCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 914

RESULT 10
US-09-181-585-1

; Sequence 1, Application US/09181585
; Patent No. 6524791
; GENERAL INFORMATION:
; APPLICANT: Rannum, Laura P.W.
; APPLICANT: Koob, Michael
; TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
; FILE REFERENCE: 1100900101
; CURRENT APPLICATION NUMBER: US/09/181,585
; CURRENT FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1159
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-181-585-1

Query Match 9.9%; Score 100; DB 4; Length 1159;
Best Local Similarity 56.8%; Pred. No. 7e-15;
Matches 184; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

Qy 406 TCCCTTAGCTACTCAGTGAATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 465
Db 403 TCCCTTAGCTAGACCTGGGCTCTTATGTAAGAAACCTGGCTTACTACTACTACTAC 462
Qy 466 TCCCTTAGCTTTTTCAGACGCTGACAGACCGCTGCCCCACTATTGACGCTGAGCC 525
Db 463 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 522

QY 526 TGTGTCAGCTGACCTTTACAGCCACCTGTAGAGCTGAGCTGTCAGAGGAGCC 585
DB 523 TGTGTCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 582
QY 586 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 645
DB 583 TGTGTCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 642
QY 646 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 705
DB 643 TGTGTCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 702
QY 706 TTTACAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 729
DB 703 TGTGTCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726

RESULT 11

US-09-181-585-2
; Sequence 2, Application US/09181585
; Patent No. 6524791
; GENERAL INFORMATION:
; APPLICANT: Ramum, Laura P.W.
; TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
; FILE REFERENCE: 1100900101
; CURRENT APPLICATION NUMBER: US/09/181,585
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA
US-09-181-585-2

Query Match 9.9%; Score 100; DB 4; Length 1471;
Best Local Similarity 56.8%; Pred. No. 7.8e-15;
Matches 184; Conservative 0; Mismatches 140; Indels 0; Gaps 0;
QY 406 TCCCTAGCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 465
DB 1025 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1084
QY 466 TCCCTAGCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 525
DB 1085 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1144
QY 526 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 585
DB 1145 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1204
QY 586 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 645
DB 1205 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1264
QY 646 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 705
DB 1265 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1324
QY 706 TTTACAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 729
DB 1325 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1348

RESULT 12
US-09-253-691-3/c
; Sequence 3, Application US/09253691
; Patent No. 6124100

; GENERAL INFORMATION:
; APPLICANT: Dong Kyu JIN
; TITLE OF INVENTION: Diagnostic Method and Kit for Neuropsychiatric Diseases
; TITLE OF INVENTION: Using Trinucleotide Repeats Sequence
; FILE REFERENCE: 1942/36
; CURRENT APPLICATION NUMBER: US/09/253,691
; EARLIER FILING DATE: 1999-02-22
; EARLIER APPLICATION NUMBER: KR 98-6,278
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: WordPerfect 6.1/Windows
; SEQ ID NO 3
; LENGTH: 397
; TYPE: DNA
; ORGANISM: human
US-09-253-691-3

Query Match 9.3%; Score 93.6; DB 3; Length 397;
Best Local Similarity 62.3%; Pred. No. 1.5e-13;
Matches 147; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 481 TTTACAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 354 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 295
QY 541 TTTACAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 294 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 235
QY 601 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 234 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 175
QY 661 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 716
DB 174 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 119

RESULT 13

5273901-6/c
; Patent No. 5273901
; APPLICANT: JACOBSON, JAMES W.; STRAUSSBERG, ROBERT L.; WILSON,
; SUSAN D.; POSE, SHARON H.; STRAUSSBERG, SUSAN L.; RUFF, MICHAEL D.;
; AUGUSTINE, PATRICIA C.; DANFORTH, HARRY D.
; TITLE OF INVENTION: GENETICALLY ENGINEERED COCCIDIOSIS
; SORBOZOITE 21.5 KB ANTIGEN, AC-6B
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/581,693
; FILING DATE: 12-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 215,162
; FILING DATE: 05-JUL-1988
; APPLICATION NUMBER: 746,520
; FILING DATE: 19-JUN-1985
; APPLICATION NUMBER: 627,811
; FILING DATE: 05-JUL-1984
; SEQ ID NO: 6
; LENGTH: 543
5273901-6

Query Match 9.1%; Score 92; DB 6; Length 543;
Best Local Similarity 54.4%; Pred. No. 4.2e-13;
Matches 185; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 430 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 489
DB 354 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 295
QY 490 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 549
DB 294 TGTTCAGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 235

QY 550 CACACCTGTGAGAGCTGAGCCTGTGACAGGAGCCCTGTGTGAGCTGAGCCTGTGACAGA 609
DB 234 TGTCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGC 175
QY 610 GGCACCTGTGTGAGAGCCTGTGTGACAGGCACTGTGTGAGCTGTGAGCCTGTGTGACAGA 669
DB 174 TGTCTGTGTGAGAGCTGTGTGAGCTGTGTGAGCTGTGTGAGCTGTGTGAGCTGTGTGAGC 115
QY 670 GGCACCTGTGTGAGAGCTGTGTGAGCTGTGTGAGCTGTGTGAGCTGTGTGAGCTGTGTGAGC 729
DB 114 TGTCTGTGAGCTGTGAGCTGTGTGAGCTGTGTGAGCTGTGTGAGCTGTGTGAGCTGTGTGAGC 55
QY 730 CAGCCTGTGTGAGCTGTGTGAGCTGTGTGAGCTGTGTGAGCTGTGTGAGCTGTGTGAGC 769
DB 54 TGTCTGT 15

RESULT 14

US-08-469-802B-3/c
Sequence 3, Application US/08469802B
Patent No. 5741645
GENERAL INFORMATION:
APPLICANT: Orr, Harry T.
APPLICANT: Rannum, Laura P.W.
APPLICANT: Chung, Ming-Yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueeling, Raasch, Gebhardt & Schwappach, P.A.
STREET: 119 No. 5741645th Fourth Street, Suite 203
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueeling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00030101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1225
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-469-802B-3

Query Match 8.7%; Score 87.6; DB 1; Length 234;

Best Local Similarity 63.1%; Pred. No. 3.2e-12;

Matches 135; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

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US-08-267-803B-3/c
Sequence 3, Application US/08267803B
Patent No. 5834183
GENERAL INFORMATION:
APPLICANT: Orr, Harry T.
APPLICANT: Rannum, Laura P.W.
APPLICANT: Chung, Ming-Yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueeling, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-267-803B-3

Query Match 8.7%; Score 87.6; DB 2; Length 234;

Best Local Similarity 63.1%; Pred. No. 3.2e-12;

Matches 135; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 482 TGAGAGCTGTGAGACCCGCTGCTCCCACTATTGACGTGAGCTGTGAGCTGTGAGCT 541
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us-09-923-236-1.rn1

Page 8

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Job time : 92 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 16, 2004, 08:42:28 ; Search time 392 Seconds
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Perfect score: 1008
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Gapop 10.0 , Gapept 1.0

Searched: 2324096 seqs, 1762381658 residues

Total number of hits satisfying chosen parameters: 4648192

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 10: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
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- 13: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
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- 17: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1008	100.0	1008	10	US-09-922-469-1
4	981.6	97.4	1325	11	US-09-746-783-105
5	896.4	88.9	959	13	US-10-231-417-41
6	460	45.6	657	9	US-09-922-480-3
7	460	45.6	657	9	US-09-923-236-3
8	460	45.6	657	10	US-09-922-469-3
9	121.2	12.0	3489	13	US-10-294-804-1
10	100	9.9	1037	12	US-10-373-667-3
11	100	9.9	1159	12	US-10-373-667-1
12	100	9.9	1471	12	US-10-373-667-2
13	98.2	9.7	2108	10	US-09-962-832-225
14	92.4	9.2	1101	9	US-09-874-062-2
15	89.2	8.8	2183	12	US-10-104-047-1064

C 16	87.6	8.7	1101	9	US-09-874-062-2	Sequence 2, App11
C 17	85.2	8.5	1926	13	US-10-294-804-3	Sequence 3, App11
C 18	85.2	8.5	8705	15	US-10-291-230-14	Sequence 14, App1
C 19	85.2	8.5	8705	15	US-10-291-249-14	Sequence 14, App1
C 20	85.2	8.5	9600	13	US-10-278-751-1	Sequence 1, App11
C 21	85.2	8.5	10233	13	US-10-050-899-283	Sequence 283, App
C 22	85.2	8.5	10285	13	US-10-050-902-283	Sequence 283, App
C 23	84	8.3	1037	12	US-10-373-667-3	Sequence 3, App11
C 24	84	8.3	1159	12	US-10-373-667-1	Sequence 1, App11
C 25	84	8.3	1471	12	US-10-373-667-2	Sequence 2, App11
C 26	83.6	8.3	477	13	US-10-357-322-1	Sequence 1, App11
C 27	83	8.2	2183	12	US-10-104-047-1064	Sequence 1064, App
C 28	78.2	7.8	16482	12	US-10-374-077-208	Sequence 208, App
C 29	77.8	7.7	422	10	US-09-738-973-337	Sequence 337, App
C 30	77.8	7.7	422	10	US-09-854-133-337	Sequence 337, App
C 31	77.8	7.7	422	15	US-10-144-644A-337	Sequence 337, App
C 32	75	7.4	14859	12	US-10-051-874-55	Sequence 55, App1
C 33	73.4	7.3	9369	13	US-10-200-562-190	Sequence 190, App
C 34	73.4	7.3	9369	13	US-10-237-551-190	Sequence 190, App
C 35	73.4	7.3	9369	13	US-10-237-551-247	Sequence 247, App
C 36	73.4	7.3	15476	13	US-09-827-688-8	Sequence 8, App11
C 37	73.2	7.3	14659	12	US-10-051-874-55	Sequence 55, App1
C 38	72.6	7.2	1388	12	US-10-264-049-518	Sequence 518, App
C 39	72.2	7.2	469	13	US-10-029-386-20613	Sequence 20613, A
C 40	72.2	7.2	5379	15	US-10-128-714-5305	Sequence 5305, App
C 41	71.8	7.1	2404	12	US-10-104-047-1740	Sequence 1740, App
C 42	71.8	7.1	3439	12	US-10-161-927-53	Sequence 53, App1
C 43	71.6	7.1	628	13	US-10-029-386-22859	Sequence 22859, A
C 44	71.6	7.1	1008	9	US-09-922-480-1	Sequence 1, App11
C 45	71.6	7.1	1008	9	US-09-923-236-1	Sequence 1, App11

ALIGNMENTS

RESULT 1
US-09-922-480-1
; Sequence 1, Application US/09922480
; Patent No. US20020081701A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZS1G63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/922,480
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)...(784)
US-09-922-480-1

Query Match 100.0%; Score 1008; DB 9; Length 1008;
Best Local Similarity 100.0%; Pred. No. 1.1e-236;
Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	AGCAGACCTAAAGGCGATGTTCTTCTCTTAAAGAGAAATATTAAT	60
QY	61	TAAATATGATGCGATTTCTTAAACATTAATTAATAGTTATATTCAGGTC	120
DB	61	TAAATATGATGCGATTTCTTAAACATTAATTAATAGTTATATTCAGGTC	120
QY	121	AATCAATGAAAGCTTCTCTTGGGCTGCAATGATATGTGCTTTGCAAGAGAG	180
DB	121	AATCAATGAAAGCTTCTCTTGGGCTGCAATGATATGTGCTTTGCAAGAGAG	180

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Db      121 AATCAAAATGAAGCTTCTCTTGGGCGCTGACATGATGTGTGCTTTGCAAGAAAG 180
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Qy      241 GAATATTCCTTAATGAGATGAGAAATTTACCACTTCTTTATTAATGAGAAATAC 300
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Db      301 AGTCCCAAGTTACCTGGAATATCTTAACAGACAGAGTTACCTGTATCCCTGAT 360
Qy      361 TCTAATCTTCTCTGATTCCTCTATGTCTATCAGATCCGTGTGTTCCCTTACTCA 420
Db      361 TCTAATCTTCTCTGATTCCTCTATGTCTATCAGATCCGTGTGTTCCCTTACTCA 420
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Qy      481 TTCAAGAGCTGAGACCCGCTGCTCCACCTATTCAGAGCTGAGCTGAGCTGACC 540
Db      481 TTCAAGAGCTGAGACCCGCTGCTCCACCTATTCAGAGCTGAGCTGAGCTGACC 540
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RESULT 2
US-09-923-236-1
; Sequence 1, Application US/09923236
; Patent No. US20020090677A1
; GENERAL INFORMATION:
; APPLICANT: Shepard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZS163 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/923,236
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 9

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128) ... (784)
US-09-923-236-1

Query Match      100.0%; Score 1008; DB 9; Length 1008;
Best Local Similarity 100.0%; Pred. No. 1..1e-236;
Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AGACAGCTAAAGGACATGATTTCTTGTGTTCTCTCTTAAAGAAAGAAATATAAT 60
Db      1 AGACAGCTAAAGGACATGATTTCTTGTGTTCTCTCTTAAAGAAAGAAATATAAT 60
Qy      61 TAAATATACATGCGTATTTCTTAAACATTAATTAATGTTAATTAATTCATAGGTC 120
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Qy      121 AATCAAAATGAAGCTTCTCTTTGAGCTGATGATGATGTTGCTTTTGCAGAAAG 180
Db      121 AATCAAAATGAAGCTTCTCTTTGAGCTGATGATGATGTTGCTTTTGCAGAAAG 180
Qy      181 ACGGTTCCTTCATTTGAGAGATGACAAATGAGATGTACCCACTTCAATCTCT 240
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Qy      241 GAATATTCCTTAATGAGATGAGAAATTTACCACTTCTTTATTAATGAGAAATAC 300
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Qy      301 AGTCCCAAGTTACCTGGAATATCTTAACAGACAGAGTTACCTGTATCCCTGAT 360
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Qy      361 TCTAATCTTCTCTGATTCCTCTATGTCTATCAGATCCGTGTGTTCCCTTACTCA 420
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Qy      421 GTTGAATGTTCTCTCTCTCTCTCTAGGGGTTTCCGTTTGTCTCTCTCAAGTTT 480
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RESULT 3

US-09-922-469-1
 ; Sequence 1, Application US/09922469
 ; Patent No. US20020173027A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Adler, David A.
 ; TITLE OF INVENTION: SECRETED SALLIVARY ZSTIG63 POLYPEPTIDE
 ; FILE REFERENCE: 97-71
 ; CURRENT APPLICATION NUMBER: US/09/922,469
 ; CURRENT FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: US 60/124,820
 ; PRIOR FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1008
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (128) ... (784)
 ; US-09-922-469-1

Query Match 100.0%; Score 1008; DB 10; Length 1008;

Best Local Similarity 100.0%; Pred. No. 1.1e-236; Indels 0; Gaps 0;

Matches 1008; Conservative 0; Mismatches 0;

QY 1 AGACAGACTAAAAAGCCATGATTTCTTGTCTCTCTAAAAAGAAAAATATATAT 60
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 QY 481 TTGAGAGCTGAG 540
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QY 541 TCTTACAGCCACACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
 DB 541 TCTTACAGCCACACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
 QY 601 TCTTACAGCCACACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 DB 601 TCTTACAGCCACACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 QY 661 TCTTACAGCCACACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 DB 661 TCTTACAGCCACACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
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 DB 721 TCTTACAGCCACACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 QY 781 TCTTACAGCCACACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 DB 781 TCTTACAGCCACACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 QY 841 GAAATCTACAAAAGTTTCTTCTTTTCCAAAGACTATTTCATTCGTGTATTCAGAGT 900
 DB 841 GAAATCTACAAAAGTTTCTTCTTTTCCAAAGACTATTTCATTCGTGTATTCAGAGT 900
 QY 901 ATTCACTCAGTACATGATTTGTTGTGAGTCTTTCTTGAGCTTAATTATATGA 960
 DB 901 ATTCACTCAGTACATGATTTGTTGTGAGTCTTTCTTGAGCTTAATTATATGA 960
 QY 961 AAAACATTGATTAATTAATAATTAATGATTAATTAGACCAATGG 1008
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RESULT 4

US-09-746-783-105

; Sequence 105, Application US/09746783

; Publication No. US2003004935A1

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

; McCoy, John M.

; Lavallie, Edward R.

; Racie, Lisa A.

; Treacy, Maurice

; Spaulding, Vikki

; Agostino, Michael J.

; Howes, Steven H.

; Fehrl, Kim

; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

; NUMBER OF SEQUENCES: 231

; CORRESPONDENCE ADDRESS:

; ADDRESS: Genetics Institute, Inc.

; STREET: 87 Cambridge Park Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: U.S.A.

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/746,783

; FILING DATE: 21-Dec-2000

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Milasincic, Debra J.

; REGISTRATION NUMBER: 46,931

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 742-4214


```

QY 672 CACCTGTTGAGTGAAGCAGCTGACAGAACTTCAACAGCTGAGCTGCTACAGCA 731
DB 612 CACCTGTTGAGTGAAGCAGCTGACAGAACTTCAACAGCTGAGCTGCTACAGCA 671
QY 732 AGCTGCTGCCCCAGAACTCAACCTTCTCTCTCTTGAACAGCAATCAAGTAATT 791
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DB 732 CTTGGAAGAGTACCAATGGTTCATTTCTATCTAGTGAAGAAATAGTAATCTACAA 791
QY 852 AAGTTTCTTCTTCTTCCAAAGACTATTTCAATCTGTGATTCAGAGTATTCATCTCAC 911
DB 792 AAGTTTCTTCTTCTTCCAAAGACTATTTCAATCTGTGATTCAGAGTATTCATCTCAC 851
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RESULT 6

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US-09-922-480-3
/ Sequence 3, Application US/09922480
/ Patent No. US20020081701A1
/ GENERAL INFORMATION:
/ APPLICANT: Sheppard, Paul O.
/ APPLICANT: Adler, David A.
/ TITLE OF INVENTION: SECRETED SALIVARY ZS1G63 POLYPEPTIDE
/ FILE REFERENCE: 97-71
/ CURRENT APPLICATION NUMBER: US/09/922,480
/ CURRENT FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: US 60/124,820
/ PRIOR FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 3
/ LENGTH: 657
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Degenerate polynucleotide sequence for zsi63
/ NAME/KEY: misc.feature
/ LOCATION: (1)...(657)
/ OTHER INFORMATION: n = A,T,C or G
US-09-922-480-3

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Query Match 45.6%; Score 460; DB 9; Length 657;

Best Local Similarity 61.0%; Pred. No. 1.9e-102; Matches 401; Conservative 103; Mismatches 153; Indels 0; Gaps 0;

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QY 128 ATGAAGCTTCTCTTGGGCGCTGATGTATGTTGCTTTGCAAGGAAGAGCGTTTC 187
DB 1 ATGAATTTTNTTNTTGGGCGTGTATGTTGTGTCGTCGNNGNARNGMNTT 60
QY 188 CCCTTCATTGTGAGATGACATGACGATGTACCCACTTCATCCATCTCTGAATATT 247
DB 61 CATTATATGAGNARGAYGAAYAGAYGAGCAVCNTYTACVCCMNSNTTAAAYATH 120
QY 248 CCTTATGCAATACGAATTTACCACTCTCTTATATATGCCCCAGTAATACAGTCCC 307
DB 121 CCAATGAGATGNAAYATTCNCCNCNTYTATATATGNCNGTNAAYACNGTNCN 180
QY 308 AGTTACCCCTGGGAATCTTACACTGACACAGGGTTACCTGATCCCTGGATTCTAAT 367
DB 181 WNTATACCGNAAAYACNTATACNGAYACNGAYTTCMNSNTATCCNTGATHYTNACN 240
QY 368 TCTCCTGATTCCTCATGTCTATCAATCCGTGGTTCCTTACCTACTCAGTTGAAT 427

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DB 241 WNTCCNGNTTTCNTATATGNTATYCAVATHMNGNTTTCNTYTGNCNACNARYTNAY 300
QY 428 GTTCTCTCTCCCTCCCTTGAAGGGGTTTCCGTTTGTCCCTCCCTCAAGGTTTTTCAGA 487
DB 301 GTTCCNCCNTYTNCNCCNNGNNTTTCNTYTGTNCNCCMNSMNTTITTYMNGCN 360
QY 488 GCTGACGACCCGCTGCCCACTTATGAGCTGAGCTGCTGAGCTGACCTCTTACA 547
DB 361 GNGNNGNCCNCGNCGNCCNCAATHGNGNARGARCCNCGNCGNCGNCCNTYNACN 420
QY 548 GCCACACTGTATGACAGCTGAGCTGCTGAGGGGCCCTGTGTGACAGCTGAGCTGCA 607
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QY 608 GAGGACCTGTTGAGCTGAGCTGCTGCTGACAGGACCTGTTGACAGCTGAGCTGCA 667
DB 481 GARGNCCNGTNGGNGCNGARCCNCGNCGNARGNCCNGTNGCNGCNGARCCNCGNCGN 540
QY 668 GAGGACCTGTTGAGCTGAGCTGAGCTGACAGGAACTTCAACAGCTGAGCTGCTACA 727
DB 541 GARGNCCNGTNGGNGTNGARCCNCGNCGNARGARCCMNSMNTTITTYMNGCN 600
QY 728 GCCAAGCTGCTGCCCCGAGAACTTCAACCTTCTCTCTCTTGAACAGGCAATTCAG 784
DB 601 GCNAARCCNGNCCNCGNARGARCCNCAVCCMNSMNTTITTYMNGARCCNCAAYCAR 657

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RESULT 7

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US-09-923-236-3
/ Sequence 3, Application US/09923236
/ Patent No. US20020090677A1
/ GENERAL INFORMATION:
/ APPLICANT: Sheppard, Paul O.
/ APPLICANT: Adler, David A.
/ TITLE OF INVENTION: SECRETED SALIVARY ZS1G63 POLYPEPTIDE
/ FILE REFERENCE: 97-71
/ CURRENT APPLICATION NUMBER: US/09/923,236
/ CURRENT FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: US 60/124,820
/ PRIOR FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 3
/ LENGTH: 657
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Degenerate polynucleotide sequence for zsi63
/ NAME/KEY: misc.feature
/ LOCATION: (1)...(657)
/ OTHER INFORMATION: n = A,T,C or G
US-09-923-236-3

```

Query Match 45.6%; Score 460; DB 9; Length 657;

Best Local Similarity 61.0%; Pred. No. 1.9e-102; Matches 401; Conservative 103; Mismatches 153; Indels 0; Gaps 0;

```

QY 128 ATGAAGCTTCTCTTGGGCGCTGATGTATGTTGCTTTGCAAGGAAGAGCGTTTC 187
DB 1 ATGAATTTTNTTNTTGGGCGTGTATGTTGTGTCGTCGNNGNARNGMNTT 60
QY 188 CCCTTCATTGTGAGATGACATGACGATGTACCCACTTCATCCATCTCTGAATATT 247
DB 61 CATTATATGAGNARGAYGAAYAGAYGAGCAVCNTYTACVCCMNSNTTAAAYATH 120
QY 248 CCTTATGCAATACGAATTTACCACTCTCTTATATATGCCCCAGTAATACAGTCCC 307
DB 121 CCAATGAGATGNAAYATTCNCCNCNTYTATATATGNCNGTNAAYACNGTNCN 180
QY 308 AGTTACCCCTGGGAATCTTACACTGACACAGGGTTACCTGATCCCTGGATTCTAAT 367
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Db      754 CTACTGGGGCTGCTGCTGCTGCTGCTGAGACTACTGCTGGGGCTGCTGCTGAGACTG 695
QY      501 CTGCCCCACCTATTGACGCTGAGGCTGTCGACGTCGACCTCTTACAGCCACACTGTAG 560
Db      694 CTACTGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 635
QY      561 CAGCTGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 620
Db      634 CTGCTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 575
QY      621 GAGCTGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 680
Db      574 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 515
QY      681 GAGTGAAGCCAGCTGACAGAGAACCTTACACAGCTGAGCCTGCTACAGCCAGCCTGCTG 740
Db      514 AGGATGCTGCTGCTGAGGATGCTTCTGAGCTGCTGAGCTGCTGCTGCTGCTGCTGCTG 455
QY      741 CC 742
Db      454 CC 453
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Search completed: January 16, 2004, 10:30:01
Job time : 397 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 16, 2004, 07:13:18 ; Search time 2130 Seconds
(without alignments)
11501.837 Million cell updates/sec

Title: US-09-923-236-1
Perfect score: 1008
Sequence: 1 agacagactcaaaaagccat.....tagataatcagcaatg 1008

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estda:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	703	69.7	703	2	HS075873	Bx485686 Homo sapi
2	680.4	67.5	682	14	HS076010	Bx485823 Homo sapi
3	677.4	67.2	742	14	CB957562	CB957562 AGENCOURT
4	667	66.2	677	2	HS075890	Bx485703 Homo sapi

5	655	65.0	659	2	HS075629	Bx485442 Homo sapi
6	655	65.0	677	2	HS076867	Bx486680 Homo sapi
7	654.6	64.9	675	2	HS076755	Bx486568 Homo sapi
8	647	64.2	675	2	HS076748	Bx486561 Homo sapi
9	641.4	63.6	665	2	HS075590	Bx485403 Homo sapi
10	640.4	63.5	678	2	HS077932	Bx487745 Homo sapi
11	633.4	62.8	647	2	HS077857	Bx487670 Homo sapi
12	614.2	60.9	672	2	HS074459	Bx484273 Homo sapi
13	605	60.0	658	2	HS075827	Bx485640 Homo sapi
14	603.4	59.9	618	2	HS074630	Bx484444 Homo sapi
15	585.4	58.1	610	2	HS075337	Bx485150 Homo sapi
16	562	55.8	573	2	HS076631	Bx485444 Homo sapi
17	549.4	54.5	572	2	HS076126	Bx485934 Homo sapi
18	541.8	53.8	572	2	HS074549	Bx484363 Homo sapi
19	519	51.5	531	2	HS076365	Bx486778 Homo sapi
20	516.8	51.3	531	2	HS076729	Bx486542 Homo sapi
21	490.6	48.7	542	2	HS081001	Bx509214 Homo sapi
22	483.8	48.0	498	2	HS076978	Bx486791 Homo sapi
23	483.8	48.0	503	2	HS076402	Bx486215 Homo sapi
24	475	47.2	491	2	HS076125	Bx485938 Homo sapi
25	467.8	46.4	483	2	HS075308	Bx485121 Homo sapi
26	451	44.7	514	2	HS075124	Bx484937 Homo sapi
27	433.6	43.0	449	2	HS076457	Bx486270 Homo sapi
28	403.8	40.1	504	2	HS076054	Bx485867 Homo sapi
29	394	39.1	405	2	HS077483	Bx487296 Homo sapi
30	299	29.7	289	2	HS077075	Bx486888 Homo sapi
31	258.2	25.6	437	2	HS077573	Bx487386 Homo sapi
32	227	22.5	227	2	HS074843	Bx484657 Homo sapi
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34	178.2	17.7	682	2	HS075684	Bx485497 Homo sapi
35	153	15.2	1302	11	AK015291	AK015291 Mus muscu
36	133	13.2	499	10	BF544627	BF544627 UI-R-BTO-
37	131.2	13.0	492	28	AQ133079	AQ133079 HS 2188 A
38	131	13.0	926	14	BT14849	BT14849 BT14849
39	125.8	12.5	711	12	BM934267	BM934267 UI-M-CGOp
40	109.6	10.9	700	14	CA510498	CA510498 UI-R-FJO-
41	109.6	10.9	754	14	CA512401	CA512401 UI-R-FJO-
42	109.6	10.9	756	14	CA512995	CA512995 UI-R-FJO-
43	108	10.7	594	14	CB584404	CB584404 AMGNUG.M
44	108	10.7	605	28	AZ640388	AZ640388 1M0502E21
45	108	10.7	718	28	AZ572907	AZ572907 2M0246M24

ALIGNMENTS

RESULT 1
ID HSM075873 standard; RNA; EST; 703 BP.
XX HSM075873
AC Bx485686;
SV Bx485686.1
DT 09-MAY-2003 (Rel. 75, Created)
DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp686C15248_r1 (from clone DKFZp686C15248)
XX EST; expressed sequence tag.
XX Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX [1]
RP 1-703
RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Mewes H.W., Well B.,
RA Amid C., Oeanger A., Fobo G., Han M., Wiemann S.,
RT Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
RL MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
XX

	XX	This is the 5' sequence of the clone insert
	CC	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
	CC	Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
	CC	sequenced by Medigenomix (Martinsried/Germany) within the cDNA
	CC	No 61 sequence available.
	CC	This clone (DKFZ686C15248) is available at the RZPD in Berlin.
	CC	Please contact the RZPD; Ressourcenzentrum, Heubnerweg 6,
	CC	14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
	FH	Key Location/Qualifiers
	FT	source
	FT	1. 703
	FT	/db_xref="taxon:9606"
	FT	/mol_type="mRNA"
	FT	/organism="Homo sapiens"
	FT	/clone="DKFZ686C15248"
	FT	/name="lib=686 (synonym: hlec3). Vector pSport1_sfi; host:
	FT	DH10B; sites =SfiI + SfiIB"
	FT	/dev_stage="adult"
	FT	/issue_type="cDNA-collection"
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SQ	Sequence 703 BP; 158 A; 195 C; 151 G; 199 T; 0 other;	
	Query Match 69.7%; Score 703; DB 2; Length 703;	
	Best Local Similarity 100.0%; Pred.No. 1,1e-103;	
	Matches 703; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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DB	1 TCTAAAGAAGAAAAATTAATTAAATTAACATTCGGTATTTCTTAAAACAATAAATTT 60	
OY	98 ATAGGTAAATTCATAGGGGCATCAATCAAAATGAAGCTTCTCTTGCGGCGCATTTGA 157	
DB	61 ATAGGTAAATTCATAGGGGCATCAAAATGAAGCTTCTCTTGCGGCGCATTTGA 120	
OY	158 TGCTGTGCTTTTGCAGAGAGAGACGGTTCCTTCATTTGGTGAAGATGACATGACAT 217	
DB	121 TGCTGTGCTTTTGCAGAGAGAGACGGTTCCTTCATTTGGTGAAGATGACATGACAT 180	
OY	218 GGTCACCACATTCATTCATCTCTGAATATTCCTTANAGCATACGGAAATTATACACTCCT 277	
DB	181 GGTCACCACATTCATTCATCTCTGAATATTCCTTANAGCATACGGAAATTATACACTCCT 240	
OY	278 CTATTATATGCCAGTAGAATACAGTCCCAGATTACCCCTGGAAATACCTTACATGACACA 337	
DB	241 CTATTATATGCCAGTAGAATACAGTCCCAGATTACCCCTGGAAATACCTTACATGACACA 300	
OY	338 GGGTAACTTCGTATCCCCGTGAATCTTACTCGATATCCCTATATGTCTATGACATC 397	
DB	301 GGGTAACTTCGTATCCCCGTGAATCTTACTCGATATCCCTATATGTCTATGACATC 360	
OY	398 CGTGGTTTTCCCTTGAAGTACTCAGTGTGATGTTCCTCTCTCCCTCCTAGAGGGTTTTCCG 457	
DB	361 CGTGGTTTTCCCTTGAAGTACTCAGTGTGATGTTCCTCTCTCCCTCCTAGAGGGTTTTCCG 420	
OY	458 TTGTGTCCTCTCTTCAAAGTTTTTTTTCAGAGCTGACAGCACCCGCTGCCACCTATTTGGA 517	
DB	421 TTGTGTCCTCTCTTCAAAGTTTTTTTTCAGAGCTGACAGCACCCGCTGCCACCTATTTGGA 480	
OY	518 GGTAGACCTGCTGACAGCTGCACCTCTTACAGCACACCTGTNAGACGTAGAGCTGTGCA 577	
DB	481 GGTAGACCTGCTGACAGCTGCACCTCTTACAGCACACCTGTNAGACGTAGAGCTGTGCA 540	
OY	578 GGGGCCCCCTGTGACAGCTGAGGCTGTGTGACAGGACACCTGTTGAGCTGAGGCTGTGCA 637	
DB	541 GGGGCCCCCTGTGACAGCTGAGGCTGTGTGACAGGACACCTGTTGAGCTGAGGCTGTGCA 600	
OY	638 GAGGGAACCTGTGACAGCTGAGGCTGTGTGACAGGACACCTGTTGAGCTGAGGCACTGTGA 697	
DB	601 GAGGGAACCTGTGACAGCTGAGGCTGTGTGACAGGACACCTGTTGAGCTGAGGCACTGTGA 660	
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Df		661 GAGGAACCTTCACCAGCTGAGCGCTGCATCAAGCCAAAGCCTGTG	703
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ID	HSM076010	standard; RNA; EST; 682 BP.	
XX	BM076010		
XX	BM485823;		
SV	BX485823.1		
DT	09-MAY-2003 (Rel. 75, Created)		
DT	09-MAY-2003 (Rel. 75, Last updated, Version 1)		
DE	Homo sapiens mRNA; EST DKFZP686L06248_r1 (from clone DKFZP686L06248)		
XX			
XX	EST; expressed sequence tag.		
XX			
OS	Homo sapiens (human)		
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia		
OC	Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
XX	[1]		
RN	Ottenwajder B., Obermaier B., Deutschenbauer S., Mewes H.W., Weil B.,		
RA	Amd C., Oeinger A., Robo G., Han M., Wiemann S.;		
RT	Submitted (07-MAY-2003) to the EMBL/GenBank/DDBJ databases.		
RL	MPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY		
XX	This is the 5' sequence of the clone insert		
CC	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer		
CC	Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;		
CC	sequenced by Medigenomix (Martinsried/Germany) within the CDNA		
CC	sequencing consortium of the German Genome Project.		
CC	No. 81 sequence available.		
CC	This clone (DKFZP686L06248) is available at the RZPD in Berlin.		
CC	Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,		
CC	14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de		
PH	Key	Location/Qualifiers	
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FT	/mol_type="mRNA"		
FT	/organism="Homo sapiens"		
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FT	/clove_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host		
FT	DHIOB; sites SfIIR + SfIIB"		
FT	/dev_stage="adult"		
FT	/issue_type="CDNA-collection"		
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Query Match	67.5%; Score 680.4; DB 2; Length 682;		
Best Local Similarity	99.9%; Pred. No. 4.9e-100;		
Matches 681; Conservative	0; Mismatches 1; Indels 0; Gaps 0;		
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QY	TGCGTATTTCCTAATAACAATTAATTTAGTGTAATATTCATAGGGTCATCAAATGA	131	
QY	AGCTTCCTCTTGGGCCGTCATGTATGTGTTGCTTTTGCAGAAGAGAGCGTTCCCCT	191	
Df	61 AGCTTCCTCTTGGGCCGTCATGTATGTGTTGCTTTTGCAGAAGAGAGAGCGTTCCCCT	120	
QY	TCATTGGAGAGAGACAATAGCATAGGTGTCACCACTTCATTCCTCTGAATATTCCTT	251	
Df	121 TCATTGGAGAGAGACAATAGCATAGGTGTCACCACTTCATTCCTCTGAATATTCCTT	180	
QY	ATGGCATACGGAATTTACCACTTCCTCTTATATATGCCCCAGTAATACAGTCCCACTT	311	


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Db      181 ATGGCATAGGAATTACCACTCTCTTATTATGCGCCAGTAAGTAAGTCCCAAGT 240
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Db      301 CTGGATTCCCTGATGCTATCATCATCTGTTGTTTCCCTTAACTGACTGATGATGTTTC 360
Qy      432 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 491
Db      361 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Qy      492 CAGCACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 551
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Qy      552 CACCTGTAGCAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 611
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Qy      612 CACCTGTAGCAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671
Db      541 CACCTGTAGCAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Qy      672 CACCTGTAGCAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
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Qy      732 AGCGCTGCGCCGAGAACCTCA 753
Db      661 AGCGCTGCGCCGAGAACCTCA 682

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RESULT 3
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LOCUS             CB957562
DEFINITION       AGENCOURT 13785505 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30352440 5', mRNA sequence.
ACCESSION        CB957562
VERSION          CB957562.1 GI:30213679
KEYWORDS         EST.
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 742)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLOUTRECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM151 row: j column: 01
High quality sequence stop: 551.
Location/Qualifiers
1.742
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30352440"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
Site (ggccatcagcc); Site_2: Site (ggccgctcggcc);
Library is oligo-dT primed and directionally cloned. cDNA

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was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGACATTAAGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGGCGCAGATG-dt(30)-BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library."

```

BASE COUNT      172 a      203 c      154 g      213 t
ORIGIN
Query Match      67.2%; Score 677.4; DB 14; Length 742;
Best Local Similarity 98.8%; Pred. No. 1.5e-99;
Matches 714; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

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Qy      1 AGACAGACTAAAAAGCCATGATTCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
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Qy      61 TAAAAATACATTCGATTTCTTAAACATTAATTTATAGTCTTAATTTCTAGAGGCTC 120
Db      76 TAAAAATACATTCGATTTCTTAAACATTAATTTATAGTCTTAATTTCTAGAGGCTC 135
Qy      121 AATCAAAATGAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
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Qy      181 ACGGTTCCCTCATTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Db      196 ACGGTTCCCTCATTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 255
Qy      241 GAATATTCCTTAATGATAGGAAATTTACACCTCTCTTTATATGCGCCAGTGAATAC 300
Db      256 GAATATTCCTTAATGATAGGAAATTTACACCTCTCTTTATATGCGCCAGTGAATAC 315
Qy      301 AGTCCCGAGTTACCGTGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360
Db      316 AGTCCCGAGTTACCGTGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 375
Qy      361 TCTAATTCCTCTGATTCCTCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTA 420
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Db      436 GTTGAATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 495
Qy      481 TTCACAGCTGAGACACCGCGCTGCGCCACCTAATGAGCTGAGCGCTGAGCTGAGCTGAGC 540
Db      496 TTCACAGCTGAGACACCGCGCTGCGCCACCTAATGAGCTGAGCGCTGAGCTGAGCTGAGC 555
Qy      541 TCTTACAGCACAACCTGTAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGC 600
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Qy      601 TCTTACAGCACAACCTGTAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGC 659
Db      616 TCTTACAGCACAACCTGTAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGC 675
Qy      660 CTGCTGAGAGGAGCAGCTG-TTGAGTGAAGAGCAGCTGAGAGAG-CCCTTACAGAGCTGA 717
Db      676 CTGCTGAGAGAGCAGCTGTTTGAATGAACCGCTGAGAGAGACCTTCCACAGCTGA 735
Qy      718 GCC 720
Db      736 GCC 738

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RESULT 4
HSW075890
ID      HSW075890      standard; RNA; EST; 677 BP.

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XX AC BX485703;
XX SV BX485703.1
XX DT 09-MAY-2003 (Rel. 75, Created)
XX DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp686D09248_r1 (from clone DKFZp686D09248)
XX KM EST; expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Homidae; Homo.
XX [1]
XX RP 1-677
XX RA Otsenweider B., Obermaier B., Deutschenbaur S., Mewes H.W., Weill B.,
XX RA Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
XX RT Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
XX RL MIPs, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
XX CC This is the 5' sequence of the clone insert
XX CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
XX CC Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
XX CC sequenced by Medigenomix (Martinsried/Germany) within the CDNA
XX CC No. 81 sequence available.
XX CC This clone (DKFZp686D09248) is available at the RZPD in Berlin.
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
XX CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH
XX FH Key Location/Qualifiers
XX FT source 1..677
XX FT /db_xref="taxon:9606"
XX FT /mol_type="mRNA"
XX FT /organism="Homo sapiens"
XX FT /clone_id="686 (synonym: hlcc3). Vector pSport1_sfi; host
XX FT DH10B; sites SfiI + SfiIB"
XX FT /dev_stage="adult"
XX FT /tissue_type="CDNA-collection"
XX SQ Sequence 677 BP; 155 A; 184 C; 134 G; 204 T; 0 other;

Query Match 66.2%; Score 667; DB 2; Length 677;
Best Local Similarity 100.0%; Pred. No. 7e-98;
Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACGAGCTAAAGGCGATGATCTTCTTCTCTTAAAGAAAGAAATATATTTA 62
DB 11 ACGAGCTAAAGGCGATGATCTTCTTCTCTTAAAGAAAGAAATATATTTA 70
QY 63 AAAATACATGGCGATTTTCTTAAACAAATATATATGTTATATTCATAGGGTCA 122
DB 71 AAAATACATGGCGATTTTCTTAAACAAATATATATGTTATATTCATAGGGTCA 130
QY 123 TCAAAATAGAGCTTCTCTTGGGCGCTGATGTATGTGTGCTTTTTCAGAGAGAC 182
DB 131 TCAAAATAGAGCTTCTCTTGGGCGCTGATGTATGTGTGCTTTTTCAGAGAGAC 190
QY 183 GGTTCCTTCATTTGGTGAAGATGACATGAGAGAGTCAAGGCTTATCATCTCTGA 242
DB 191 GGTTCCTTCATTTGGTGAAGATGACATGAGAGAGTCAAGGCTTATCATCTCTGA 250
QY 243 ATATTCCTATGCGATGCGAATTTACCACTCTCTTATATGAGCCAGGATATACG 302
DB 251 ATATTCCTATGCGATGCGAATTTACCACTCTCTTATATGAGCCAGGATATACG 310
QY 303 TCCCGAGTTACCTCGGAAATCTACTGACACAGGGTTACCTTGTATCCCTGATTC 362

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DB 311 TCCCGAGTTACCTCGGAAATCTACTGACACAGGGTTACCTTGTATCCCTGATTC 370
QY 363 TAACTTCCTCGAATTTCCCTATATGATCATCATCCGCTGTTTCCCTACTACTAGT 422
DB 371 TAACTTCCTCGAATTTCCCTATATGATCATCATCCGCTGTTTCCCTACTACTAGT 430
QY 423 TGAATGTTCCCTCCCTCCCTCCCTAGGGGTTTCCGTTTGTCCCTCTCAAGTTTCTT 482
DB 431 TGAATGTTCCCTCCCTCCCTCCCTAGGGGTTTCCGTTTGTCCCTCTCAAGTTTCTT 490
QY 483 CAGAGCTGACGACACCGCTGCCCCACCTATTGACGCTGACCTGACCTGACCTC 542
DB 491 CAGAGCTGACGACACCGCTGCCCCACCTATTGACGCTGACCTGACCTGACCTC 550
QY 543 TTACAGCCACACCTGTAGACGCTGAGCTGTGACAGGGGCCCTGTGACGCTGAGCCTG 602
DB 551 TTACAGCCACACCTGTAGACGCTGAGCTGTGACAGGGGCCCTGTGACGCTGAGCCTG 610
QY 603 CTGACAGGACGACCTGTGAGCTGAGCTGCTGACAGAGGACCTGTTGCACTGAGCCTG 662
DB 611 CTGACAGGACGACCTGTGAGCTGAGCTGCTGACAGAGGACCTGTTGCACTGAGCCTG 670
QY 663 CTGACAG 669
DB 671 CTGACAG 677

RESULT 5
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ID HSM075629 standard; RNA; EST; 669 BP.
XX AC BX485442;
XX SV BX485442.1
XX DT 09-MAY-2003 (Rel. 75, Created)
XX DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp686D11247_r1 (from clone DKFZp686D11247)
XX FH
XX FH EST; expressed sequence tag.
XX FH Homo sapiens (human)
XX FH Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX FH Eutheria; Primates; Catarrhini; Homidae; Homo.
XX [1]
XX RP 1-669
XX RA Bahr A., Lauber J., Mewes H.W., Weill B., Amid C., Osanger A., Fobo G.,
XX RA Han M., Wiemann S.;
XX RT Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
XX RL MIPs, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
XX CC This is the 5' sequence of the clone insert
XX CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
XX CC Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
XX CC sequenced by Qigen (Hilden/Germany) within the CDNA sequencing
XX CC Consortium of the German Genome Project.
XX CC No. 81 sequence available.
XX CC This clone (DKFZp686D11247) is available at the RZPD in Berlin.
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
XX CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH
XX FH Key Location/Qualifiers
XX FT source 1..669
XX FT /db_xref="taxon:9606"
XX FT /mol_type="mRNA"
XX FT /organism="Homo sapiens"
XX FT /clone_id="DKFZp686D11247"
XX FT /clone_id="686 (synonym: hlcc3). Vector pSport1_sfi; host

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FT		/dev/strge="adult"
FT		/false_type="cdna-collection"
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SO	Query Match	65.0%; Score 655; DB 2; Length 669;
	Best Local Similarity	100.0%; Pred. No. 6.1e-96;
	Matches	655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1	AGACGACTAATAAAAGCCATGTATTCTTTGGTTCCTCTTAAGAAGAAAAATATATT 60
Db	15	AGACGACTAATAAAAGCCATGTATTCTTTGGTTCCTCTTAAGAAGAAAAATATATT 74
OY	61	TAAAATAATCATTTGGCGTATTTCTAAACAATTAATTAATAGTATAATTCAATAGGGTC 120
Db	75	TAAAATAATCATTTGGCGTATTTCTTAACAATTAATTAATAGTATAATTCAATAGGGTC 134
OY	121	AATCAAAATGAAGCTTCTCTTTGGGCGCTGCATTGTATGTGTGCTTTTGCAAAGAAAG 180
Db	135	AATCAAAATGAAGCTTCTCTTTGGGCGCTGCATTGTATGTGTGCTTTTGCAAAGAAAG 194
OY	181	ACGGTTCCTCCTTCAATGGTAGAGATGACAAATGACAGATGACACCATTATCATCTCT 240
Db	195	ACGGTTCCTCCTTCAATGGTAGAGATGACAAATGACAGATGACACCATTATCATCTCT 254
OY	241	GAAATATTCCTTATGGCATACGGAATTTACACACTCTCTTATTAATGAGCCAGTGAATAC 300
Db	255	GAAATATTCCTTATGGCATACGGAATTTACACACTCTCTTATTAATGAGCCAGTGAATAC 314
OY	301	AGTCCCCAGTTAACCTTGGGAATTACTTAACACTGACACAGGGTTACCTTGATCCTGGAT 360
Db	315	AGTCCCCAGTTAACCTTGGGAATTACTTAACACTGACACAGGGTTACCTTGATCCTGGAT 374
OY	361	TCTAATCTTCCTGGAATTCCTCTATGATCAATACATCCGATGGTTTTGCCCTAGCTACTCA 420
Db	375	TCTAATCTTCCTGGAATTCCTCTATGATCAATACATCCGATGGTTTTGCCCTAGCTACTCA 434
OY	421	GTTGAATGTTCT 480
Db	435	GTTGAATGTTCT 494
OY	481	TTTGAAGAGCTGACACACCCGCTGCCCCAACAATTAATGAGAGCTGAGCTGCTGACAC 540
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OY	541	TCTTACAGCCACACCTGTAGAGCTGAGCTGCTGCTGACAGGGGCCCTCTGTTCACTGAGCC 600
Db	555	TCTTACAGCCACACCTGTAGAGCTGAGCTGCTGCTGACAGGGGCCCTCTGTTCACTGAGCC 614
OY	601	TGCTGACAGAGGCACTGTTGAGAGCTGAGCTGCTGCTGACAGAGCACCTGTTGCACT 655
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XX	BX486680.1	
DT	09-MAY-2003	(Rel. 75, Created)
DT	09-MAY-2003	(Rel. 75, Last updated, Version 1)
DE	Homo sapiens mRNA; EST DKFZp686P12252_x1 (from clone DKFZp686P12252)	
XX	EST, expressed sequence tag.	
KW	Homo sapiens (human)	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia	
OC	Eutheria; Primates; Catarrhini; Hominidae; Homo.	

RN	[1]
RP	1-677
RA	Bahr A., Lauber J., Mewes H.W., Well B., Amid C., Osanger A., Fobo G.,
RA	Han W., Wiemann S.;
RT	i
RL	Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
RL	MRS, Ingolstaedter Landstr.1, D-85764 Neuberg, GERMANY
XX	
CC	This is the 5' sequence of the clone insert
CC	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC	Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
CC	sequenced by Oligen (Hilden/Germany) within the cDNA sequencing
CC	consortium of the German Genome Project.
CC	s1 sequence also available.
CC	This clone (DKFP668p2252) is available at the RZPD in Berlin.
CC	Please contact the RZPD: Ressourcentrum, Heubnerweg 6,
CC	14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX	
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FT	/clone_1bp="686 (synonym: hlcc3). Vector pSport1_sfi; host:
FT	DH10B, sites SfiI + SfiIB"
FT	/dev_stage="adult"
FT	/library_type="cDNA-collection"
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	Best Local Similarity 100.0%; Pred. No. 6, le-96;
	Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	10 AAAAAAGCAGTATTCCTTCGTTCTCTCAAAAGAAAATAATTATTAATAATAC 69
DB	23 AAAAAAGCAGTATTCCTTCGTTCTCTCAAAAGAAAATAATTATTAATAATAC 82
QY	70 ATTGGCATTTCTCAAACAATAAATTATAGTGTTATATTCATAGGGTCAATCAAAAT 129
DB	83 ATTGGCATTTCTCAAACAATAAATTATAGTGTTATATTCATAGGGTCAATCAAAAT 142
QY	130 GAACCTTCTCGTTGGGCTGCATTTGTATGTGTGCTTTTGCAAGAAGACGGTCCC 189
DB	143 GAACCTTCTCGTTGGGCTGCATTTGTATGTGTGCTTTTGCAAGAAGACGGTCCC 202
QY	190 CTTCATTGTGGAGATGAACAATGATGTCACCCACTTCATCTCATCTTGATATATCC 249
DB	203 CTTCATTGTGGAGATGAACAATGATGTCACCCACTTCATCTCATCTTGATATATCC 262
QY	250 TTATGCAATGAGAAATTACCACTCTCTTATATATGCCCCAGTAGAATACAGTCCAG 309
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QY	310 TTACCTTGGGAATATCTTACACTGACACAGGGTTAACCTTCGATCCCTGATTTCACTTC 369
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QY	370 TTCCTGATTTCCCTGATTTCTATGACACCGGTTTTCCCTTAGCTACTGAGTGAATGT 429
DB	383 TTCCTGATTTCCCTGATTTCTATGACACCGGTTTTCCCTTAGCTACTGAGTGAATGT 442
QY	430 TCCTCTCTCTCCCTCTTACGAGGGTTCCCGTTTGTCTCTCTTCAAGGTTTTTTCAGCAGC 489
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QY 550 CACACCTGTAGAGCTGAGCTGTCAGAGGGGCCCCCTGTTGAGCTGAGCCTGCTGCAGA 609
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QY 610 GGCACCTGTGAGCTGAGCCTGCTGCAGAGGACCTGTTGAGCTGAGCCTGCT 664
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ID HSM076755 standard; RNA; EST; 675 BP.
AC BX486568;
XX
XX BX486568.1
SV
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XX 09-MAY-2003 (Rel. 75, Created)
DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
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XX Homo sapiens mRNA; EST DKFZp686H08252_r1 (from clone DKFZp686H08252)
DE
XX EST; expressed sequence tag.
XX
XX Homo sapiens (human)
OS
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
XX
XX [1]
XX 1-675
XX Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
RT MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
XX
XX This is the 5' sequence of the clone insert
XX Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
CC sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
CC consortium of the German Genome Project.
CC No sl sequence available.
CC This clone (DKFZp686H08252) is available at the RZPD in Berlin.
CC Please contact the RZPD: Reesourcenzentrum, Heubnerweg 6,
CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
CC
XX Key Location/Qualifiers
FH
FH source 1. 675
FT /db_xref="taxon:9606"
FT /mol_type="RNA"
FT /organism="Homo sapiens"
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Query Match 64.9%; Score 654.6; DB 2; Length 675;
Best Local Similarity 99.3%; Pred. No. 7e-96;
Matches 668; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Db 123 CCCCCCTTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 182
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Db 183 TCCCTTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 242
QY 307 CAGTTACCTGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 366
Db 243 CAGTTACCTGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 302
QY 367 TTTCTCTGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 426
Db 303 TTTCTCTGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 362
QY 427 TTTCTCTGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 486
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Db 603 AGAGGACCTGATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 662
QY 727 AGCCAGAGCTGCT 739
Db 663 AGCCAGAGCTGCT 675

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AC BX486561;
XX
XX BX486561.1
SV
XX
XX 09-MAY-2003 (Rel. 75, Created)
DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
XX
XX Homo sapiens mRNA; EST DKFZp686H20252_r1 (from clone DKFZp686H20252)
DE
XX EST; expressed sequence tag.
XX
XX Homo sapiens (human)
OS
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
XX
XX [1]
XX 1-675
XX Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
RT MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY.
XX
XX This is the 5' sequence of the clone insert
XX Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
CC sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
CC consortium of the German Genome Project.
CC No sl sequence available.

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QY 301 AGTCCCGAGTTACCTGGGAATCTTACAGTACAGAGGTTACCTGGTATCCCTGGAT 360
DB 312 AGTCCCGAGTTACCTGGGAATCTTACAGTACAGAGGTTACCTGGTATCCCTGGAT 371
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DB 372 TCTAATCTCTCTGATTTCCCTATGTATATACATCCGTGGTTTCCCTTAGCTACCA 431
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DB 432 GTTGAATGTCCTCTCTCCCTCTAGAGGGTTTCCGTTTGTCCCTTCAAGTTTTT 491
QY 481 TTACAGAGTGAAGACCCGCTGCCCACTATTGCAAGTGAAGCTGTGACAGTCAAC 540
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DB 612 TGCTGACAGAGCAGCTGTGAGAGTGAAGCTGCTGACAGAGCAGCTGTGACAGT 665

RESULT 10
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XX HSM077932
AC BX487745;
SV BX487745.1
DT 09-MAY-2003 (Rel. 75, Created)
DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
DE Homo sapiens mRNA; EST DKFZp686N16258_r1 (from clone DKFZp686N16258)
XX EST; expressed sequence tag.
XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
XX [1]
RN Bahr A., Lauber J., Mewes H.W., Well B., Amid C., Osanger A., Pobo G.,
RP Han M., Wiemann S.;
RT Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
RL MIPs, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
XX This is the 5' sequence of the clone insert
CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
CC sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
CC consortium of the German Genome Project.
CC No s1 sequence available.
CC This clone (DKFZp686N16258) is available at the RZPD in Berlin.
CC Please contact the RZPD, Ressourcenzentrum, Heubnerweg 6,
CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key location/Qualifiers
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FT /mol_type="RNA"
FT /organism="Homo sapiens"
FT /clone="DKFZp686N16258"
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FT DH10B; sites SfiI + SfiIB"
FT /dev_stage="adult"
FT /issue_type="cDNA-collection"

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XX SQ Sequence 678 BP; 158 A; 180 C; 132 G; 207 T; 1 other;
Query Match 63.5%; Score 640.4; DB 2; Length 678;
Best Local Similarity 99.5%; Pred. No. 1.4e-93;
Matches 652; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 AGACAGACTAAGAAAGCAGTATCTTCTGTTTCTCTAAGAAAGAAATATATAT 60
DB 25 AGACAGACTAAGAAAGCAGTATCTTCTGTTTCTCTAAGAAAGAAATATATAT 84
QY 61 TAAATATACATTTGGTATTTTCTAATAATATATATATATATATATATATATAT 120
DB 85 TAAATATACATTTGGTATTTTCTAATAATATATATATATATATATATATATAT 144
QY 121 AATCAAAATGAAGCTTCTCTTGGGCTGATATGATGTTGTTTGAAGAAAGAG 180
DB 145 AATCAAAATGAAGCTTCTCTTGGGCTGATATGATGTTGTTTGAAGAAAGAG 204
QY 181 ACGGTTCCCTTCATTGGTAGATGACATGATGATGATGATGATGATGATGATGAT 240
DB 205 ACGGTTCCCTTCATTGGTAGATGACATGATGATGATGATGATGATGATGATGAT 264
QY 241 GAATATTCCTTATGAGCATAGGAAATTTACACCTCTCTTATATATGAGGAGTAT 300
DB 265 GAATATTCCTTATGAGCATAGGAAATTTACACCTCTCTTATATATGAGGAGTAT 324
QY 301 AGTCCCGAGTTACCTGGGAATCTTACAGTACAGAGGTTACCTGGTATCCCTGGAT 360
DB 325 AGTCCCGAGTTACCTGGGAATCTTACAGTACAGAGGTTACCTGGTATCCCTGGAT 384
QY 361 TCTAATCTCTCTGATTTCCCTATGTATATACATCCGTGGTTTCCCTTAGCTACCA 420
DB 385 TCTAATCTCTCTGATTTCCCTATGTATATACATCCGTGGTTTCCCTTAGCTACCA 444
QY 421 GTTGAATGTCCTCTCTCCCTCTAGAGGGTTTCCGTTTGTCCCTTCAAGTTTTT 480
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QY 541 TCTTACAGCAGCAGCTGTAGAGCTGAGCCTGTGCAAGAGGCGCCCTGTGAGTGAAG 600
DB 565 TCTTACAGCAGCAGCTGTAGAGCTGAGCCTGTGCAAGAGGCGCCCTGTGAGTGAAG 623
QY 601 TGCTGACAGAGCAGCTGTGAGAGTGAAGCTGCTGACAGAGCAGCTGTGACAGT 655
DB 624 TGCTGACAGAGCAGCTGTGAGAGTGAAGCTGCTGACAGAGCAGCTGTGACAGT 678

RESULT 11
HSM077857
XX HSM077857
AC BX487670;
SV BX487670.1
DT 09-MAY-2003 (Rel. 75, Created)
DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
DE Homo sapiens mRNA; EST DKFZp686G13258_r1 (from clone DKFZp686G13258)
XX EST; expressed sequence tag.
XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
XX [1]
RN 1-647
RP

```

RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Oeanger A., Fobo G.,
 RA Han M., Wiemann S.;
 RL Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
 XX
 CC This is the 5' sequence of the clone insert
 CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 CC sequenced by Olgan (Hilden/Germany) within the cDNA sequencing
 CC consortium of the German Genome Project.
 CC No sequence available.
 CC This clone (DKFZp686G13258) is available at the RZPD in Berlin.
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
 CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 CC
 XX
 XX
 FH Key Location/Qualifiers
 FT source 1. .647
 FT /db_xref="taxon:9606"
 FT /mol_type="mRNA"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp686G13258"
 FT /clone_1lb="686 (synonym: hicc3). Vector pSport1_Sfi; host
 FT DH10B; sites SfiIA + SfiIB"
 FT /dev_stage="adult"
 FT /tissue_type="cDNA-collection"
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 Best Local Similarity 99.8%; Pred. No. 1.9e-92;
 Matches 649; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AGACAGACTAAAAAGCCATGATCTTCTGTTCTCTTAAAGAGAAATTAAT 60
 DB 13 AGACAGACTAAAAAGCCATGATCTTCTGTTCTCTTAAAGAGAAATTAAT 72
 QY 61 TAAATAATCATTCGATTTCTTAAACAAATTAATTAAGTATATATCATAGGGTC 120
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 QY 121 AATCAAAATGAAGCTTCTCTTGGGCTGCAATGTATGTGCTTTGCAAGAGAG 180
 DB 133 AATCAAAATGAAGCTTCTCTTGGGCTGCAATGTATGTGCTTTGCAAGAGAG 192
 QY 181 AGGTTCCCTCATTTGAGAGAGATGACATGATGATCCATTCATCTCT 240
 DB 193 AGGTTCCCTCATTTGAGAGAGATGACATGATGATCCATTCATCTCT 252
 QY 241 GAATATTCCTTATGGCATACGAATTTACACCTCTTTATTAACGCCAGTAATAC 300
 DB 253 GAATATTCCTTATGGCATACGAATTTACACCTCTTTATTAACGCCAGTAATAC 312
 QY 301 AGTCCCACTTACCTGGGAATACCTACAGACAGAGGTTACCTTGATCCCTGAT 360
 DB 313 AGTCCCACTTACCTGGGAATACCTACAGACAGAGGTTACCTTGATCCCTGAT 372
 QY 361 TCTAATCTCTGATGATCCCTATGATCATCAATCGATGTTTCCCTTATGATCA 420
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QY 601 TCTGTCAGAGGACCTGTGAGCTGAGCTGCTG 635
 DB 613 TCTGTCAGAGGACCTGTGAGCTGAGCTGCTG 647
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 HSM074459
 ID HSM074459 standard; RNA; EST; 672 BP.
 XX
 AC BX484273;
 XX
 SV BX484273.1
 XX
 DT 09-MAY-2003 (Rel. 75, Created)
 DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
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 DE Homo sapiens mRNA; EST DKFZp686A18242_r1 (from clone DKFZp686A18242)
 XX
 XX EST; expressed sequence tag.
 KW
 XX Homo sapiens (human)
 OS
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 XX
 RN [1]
 RP 1-672
 RA Oltenevelde B., Obermaier B., Deutschenaur S., Mewes H.W., Weil B.,
 RA Amid C., Oeanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
 XX
 CC This is the 5' sequence of the clone insert
 CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 CC sequenced by MedGenomix (Martinsried/Germany) within the cDNA
 CC sequencing consortium of the German Genome Project.
 CC a1 sequence also available.
 CC This clone (DKFZp686A18242) is available at the RZPD in Berlin.
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
 CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 CC
 XX
 XX
 FH Key Location/Qualifiers
 FT source 1. .672
 FT /db_xref="taxon:9606"
 FT /mol_type="mRNA"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp686A18242"
 FT /clone_1lb="686 (synonym: hicc3). Vector pSport1_Sfi; host
 FT DH10B; sites SfiIA + SfiIB"
 FT /dev_stage="adult"
 FT /tissue_type="cDNA-collection"
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 SQ Sequence 672 BP; 156 A; 184 C; 126 G; 201 T; 5 other;
 Query Match 60.9%; Score 614.2; DB 2; Length 672;
 Best Local Similarity 98.3%; Pred. No. 2.3e-89;
 Matches 649; Conservative 0; Mismatches 8; Indels 3; Gaps 3;
 QY 1 AGACAGACTAAAAAGCCATGATCTTCTGTTCTCTTAAAGAGAAATTAAT 60
 DB 13 AGACAGACTAAAAAGCCATGATCTTCTGTTCTCTTAAAGAGAAATTAAT 72
 QY 61 TAAATAATCATTCGATTTCTTAAACAAATTAATTAAGTATATATCATAGGGTC 120
 DB 73 TAAATAATCATTCGATTTCTTAAACAAATTAATTAAGTATATATCATAGGGTC 132
 QY 121 AATCAAAATGAAGCTTCTCTTGGGCTGCAATGTATGTGCTTTGCAAGAGAG 180
 DB 133 AATCAAAATGAAGCTTCTCTTGGGCTGCAATGTATGTGCTTTGCAAGAGAG 192

OY	181	ACGGTTCCTCATTTGGATGATGACATACATGGTACCCACTTATCATCTCT	24.0
Db	193	ACGGTTCCTCATTTGGATGATGACATACATGGTACCCACTTATCATCTCT	23.2
OY	241	GAATATTCCTTATGGAATACGGAATTTACCACTCTCTTTATTTATGGCCAGTAATAC	30.0
Db	253	GAATATTCCTTATGGAATACGGAATTTACCACTCTCTTTATTTATGGCCAGTAATAC	31.2
OY	301	AGTCCCAAGTTACCTCGGGGAATCTTACACTGACAGGGTTACCTTGTAATCCCTGAT	36.6
Db	313	AGTCCCAAGTTACCTCGGGGAATCTTACACTGACAGGGTTACCTTGTAATCCCTGAT	37.2
OY	361	TCTAATCTCTCTGGAATTCCTCTATGCTATGACATCCGTGGTTTTCCCTTAGCTACTCA	42.0
Db	373	TCTAATCTCTCTGGAATTCCTCTATGCTATGACATCCGTGGTTTTCCCTTAGCTACTCA	43.2
OY	421	GTTGAATGTTCCCTCTCTCCCTCTTAGGGGTTTTCCCGTTTGTCCCTCTTCAAGTTTTT	48.0
Db	433	GTTGAATGTTCCCTCTCTCCCTCTTAGGGGTTTTCCCGTTTGTCCCTCTTCAAGTTTTT	49.2
OY	481	TTGACGAGCTGACGACACCGCTGCCCCCACTTATGACGTAGCCTGTGACGTGACCC	54.0
Db	493	TTGACGAGCTGACGACACCGCTGCCCCCACTTATGACGTAGCCTGTGACGTGACCC	55.2
OY	541	TCTTACGACCAACTGTGACAGCTGAGCTGTGACAGGGGCCCTGTTGACGTGAGCC	60.0
Db	553	TCTTACGACCAACTGTGACAGCTGAGCTGTGACAGGGGCCCTGTTGACGTGAGCC	61.2
OY	601	TGCGCGAGAGGCA - CCTGTTGAGAGTGAG - CCTGCTGACAGAGCA - CCTGTTGAGAGTGA	65.7
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XX	
AC BX485640;	
XX	
SV BX485640.1	
XX	
DT 09-MAY-2003 (Rel. 75, Created)	
DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)	
DE Homo sapiens mRNA; EST DKFZp686p12247_r1 (from clone DKFZp686p12247)	
XX	
KW EST; expressed sequence tag.	
XX	
OS Homo sapiens (human)	
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia	
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
XX	
[1]	
RP 1-658	
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Oranger A., Fobo G.,	
RL Han M., Wiemann S.;	
RT Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.	
RL MITS, Ingolstaedter Landstr.1, D-85764 Neuberg, GERMANY	
XX	
CC This is the 5' sequence of the clone insert	
CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer	
CC Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;	
CC Sequenced by Qiasen (Hilden/Germany) within the CDNA sequencing	
CC consortium of the German Genome Project.	
CC No sl sequence available.	
CC This clone (DKFZp686p12247) is available at the RZPD in Berlin.	
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,	
CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de	
XX	
EH Key	Location/Qualifiers
TH	
TF source	1. .658

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FT      /db_xref="taxon:9606"
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FT      /organism="Homo sapiens"
FT      /clone="D8P2686P1247"
FT      /clone_1kb="686 (synonym: hlcc3) . Vector pSport1_sfi, host
FT      DH10B; sites SfiIa + SfiIb"
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Matches 605; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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QY	61	TAAGAAATACATTCGGATTTTCTAAACAAATPAAATTATAGTGTAAATATTCATAGGGTC	120
Dp	114	TAAGAAATACATTCGGATTTTCTAAACAAATPAAATTATAGTGTAAATATTCATAGGGTC	173
QY	121	AATCAAAAAGAAAGCTTCTCCTTTGGGCGTGCATTTGTATGTGTGTCTTTTGGAAAGAAAG	180
Dp	174	AATCAAAAAGAAAGCTTCTCCTTTGGGCGTGCATTTGTATGTGTGTCTTTTGGAAAGAAAG	233
QY	181	ACGGTTCGCCCTTCATTTGGTAGAGATGACATAGACGATGGTCACCACTTCATCATCTCT	240
Dp	234	ACGGTTCGCCCTTCATTTGGTAGAGATGACATAGACGATGGTCACCACTTCATCATCTCT	299
QY	241	GAATATTCCTTATGCGATACGGAATTTACACCTCTCTTTATTTATGCGCCAGTAATAC	300
Dp	294	GAATATTCCTTATGCGATACGGAATTTACACCTCTCTTTATTTATGCGCCAGTAATAC	353
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Dp	354	AGTCCCAAGTTACCGTGGGAATATCTTACACGACACAGGGTTACTTCGTATCCCTGAT	413
QY	361	TCTAACTTCTCTGGAATTCGCCCTATGTCTATCACATCCGATGGTTTTCCTTAGCTACTCA	420
Dp	414	TCTAACTTCTCTGGAATTCGCCCTATGTCTATCACATCCGATGGTTTTCCTTAGCTACTCA	473
QY	421	GTTGAATGTTCTCTCTCTCCTCCTCTTAAGGGGTTTTCCCGTTGTCCCTCCCTCAAGGTTTT	480
Dp	474	GTTGAATGTTCTCTCTCTCCTCCTCTTAAGGGGTTTTCCCGTTGTCCCTCCCTCAAGGTTTT	533
QY	481	TTTCAGAGCTGACGACCCGCTGCGCCCACTAATTGACAGCTGAGGCTGCTGACGTGCACC	540
Dp	534	TTTCAGAGCTGACGACCCGCTGCGCCCACTAATTGACAGCTGAGGCTGCTGACGTGCACC	593
QY	541	TCTTACAGGCACACCTGTAGCAGCTGAGGCTGCTGACAGGGGCCCTGTGTCAGCTGAGCC	600
Dp	594	TCTTACAGGCACACCTGTAGCAGCTGAGGCTGCTGACAGGGGCCCTGTGTCAGCTGAGCC	653
QY	601	TGCTG 605	
Dp	654	TGCTG 658	

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AC BX484444;
XX
SV BX484444.1
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XX 09-MAY-2003 (Rel. 75, Created)
DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp686A01243..r1 (from clone DKFZp686A01243)

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KW EST; expressed sequence tag.
 XX Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 XX
 RN [1]
 RP 1-618
 RA Behr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fodor G.,
 RA Han M., Wiemann S.;
 RT Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Ingolstaedter Landstr.1, D-85764 Neuberg, GERMANY
 XX
 CC This is the 5' sequence of the clone insert
 CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 CC sequenced by Olgan (Hilden/Germany) within the CDNA sequencing
 CC consortium of the German Genome Project.
 CC No 81 sequence available.
 CC This clone (DKFZp686A01243) is available at the RZPD in Berlin.
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
 CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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 Best Local Similarity 99.8%; Pred. No. 1.3e-87;
 Matches 604; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AGACAGACTAAAAAGCCATGATCTTCTGTTCTCTTAAAGAAATTAATTT 60
 DB 14 AGACAGACTAAAAAGCCATGATCTTCTGTTCTCTTAAAGAAATTAATTT 73
 QY 61 TAAATATACATGCGTATTTCTTAAACATTAATTAATTAATTAATTAATTT 120
 DB 74 TAAATATACATGCGTATTTCTTAAACATTAATTAATTAATTAATTAATTT 133
 QY 121 AATCAAAATGAACTTCTCTTGGGCTGATGATGTTGCTTTGCAAGAAAG 180
 DB 134 AATCAAAATGAACTTCTCTTGGGCTGATGATGTTGCTTTGCAAGAAAG 193
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 DB 314 AGTCCAGTATTCCTGGAATATTAACATGACACAGGGTAACTTCTGATCCCTG 373
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 DB 374 TCTAACTTCTCCGATTCCTGATGATGATGATGATGATGATGATGATGATGAT 433
 QY 421 GTTGAATGTTCT 480
 DB 434 GTTGAATGTTCT 493

QY 481 TTCAGAGCTGACACCCGCTGCCCCACCTATTTGAGCTGAGCTGACCTGACC 540
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 QY 541 TCTTACAGCACACCTGTATGACAGCTGAGCTGAGGAGGAGGAGGAGGAGGAG 600
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 QY 601 TGCTG 605
 DB 614 TGCTG 618
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 XX BX485150;
 AC BX485150;
 SV BX485150.1
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 DT 09-MAY-2003 (Rel. 75, Created)
 DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
 XX
 DE Homo sapiens mRNA; EST DKFZp686A12246_r1 (from clone DKFZp686A12246)
 XX
 KW EST; expressed sequence tag.
 XX
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 XX
 RN [1]
 RP 1-610
 RA Koehler K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A., Fodor G.,
 RA Han M., Wiemann S.;
 RT Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Ingolstaedter Landstr.1, D-85764 Neuberg, GERMANY
 XX
 CC This is the 5' sequence of the clone insert
 CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 CC sequenced by BMFZ (Biomedical Research Center at the
 CC Heinrich-Heine-University, Duesseldorf/Germany) within the CDNA
 CC sequencing consortium of the German Genome Project.
 CC No 81 sequence available.
 CC This clone (DKFZp686A12246) is available at the RZPD in Berlin.
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
 CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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 FT source 1. .610
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 FT /mol_type="mRNA"
 FT /organism="Homo sapiens"
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 Best Local Similarity 99.8%; Pred. No. 1e-84;
 Matches 586; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 AAAAGCCATGATCTTCTGTTCTCTTAAAGAAATTAATTAATTAATTAATTA 70
 DB 24 AAAAGCCATGATCTTCTGTTCTCTTAAAGAAATTAATTAATTAATTAATTA 83

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QY 131 AAGCTTCTCTTTGGGCTGTGATGTATGTGCTTTTGCAGAGAGAGACGGTTCCC 190
Db 144 AAGCTTCTCTTTGGGCTGTGATGTATGTGCTTTTGCAGAGAGAGACGGTTCCC 203
QY 191 TTCAATTGGAGAGATGACATATGATGTACCCACTTCATCCATCTCTGAAATTTCC 250
Db 204 TTCATTGGAGAGATGACATATGATGTACCCACTTCATCCATCTCTGAAATTTCC 263
QY 251 TATGGCATACGGAATTTACCACTCTCTTATATACGCCAGATATACAGTCCCACT 310
Db 264 TATGGCATACGGAATTTACCACTCTCTTATATACGCCAGATATACAGTCCCACT 323
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Db 444 CCTCTCTCCCTCTAGGGGTTTCCCGTTTGTCCCTCTTCAAGGTTTTTTCAGAGCT 503
QY 491 GCAGACCCGCTGCCCACTATTTGACGTGAGCCTGTGACGTGACACTTTACAGCC 550
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